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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B A;Reference number: A81000; MUID:20175755; PMID:10710307
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 59K transcription activator -
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strain MC58.
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A;Gene: 63
C;Superfamily: varicella-zoster virus gene 63 protein; RING finger C;Keywords: DNA binding; transcription regulation; zinc finger F;4-52/Domain: RING finger homology <RNG>
F;8-46/Region: zinc finger C3HC4 motif
ferrioxamine B receptor precursor [imported] - Salmonella enterica subsp. e
(;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AC0547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable alpha-isopropyl malate synthase - Mycobacterium tuberculosis (stra C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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A;Title: The DNA sequence of equine herpesvirus-1. A;Reference number: A41831; MUID:92295566; PMID:1318606
A;Contents: annotation; possible protein-coding frames A;Note: neither amino acid nor nucleotide sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: leuA
C;Superfamily: 2-isopropylmalate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA18032.1; PID:g296013-A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-644 < COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: G70794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: G70794
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C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
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ferripyoverdine receptor
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-813 <POO>
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199 NLVRKRPT 206
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C.Species escuedances aeruginosa
C.Species escuedances aeruginosa
C.Species (07-Jul-1995 #test_change 31-Dec-2000
C.Accession: A36942; G83117
R.Ahkenbauer, R.G.; Quan, H.M.
J. Bacteriol: 176, 307-319, 1994
A.Title: FptA, the FeIII)-pyochelin receptor of Pseudomonas aeruginosa: a phenolate sid
A.Accession: A36942
A.Title: FptA, the FeIIII)-pyochelin receptor of Pseudomonas aeruginosa: a phenolate sid
A.Accession: A36942
A.Title: FptA, the FeIIII)-pyochelin receptor of Pseudomonas aeruginosa: a phenolate sid
A.Accession: A36942
A.Title: FptA, the FeIIII)-pyochelin receptor of Pseudomonas aeruginosa: a phenolate sid
A.Accession: A36942
A.Title: Tool ANK:
A.Reference number: A36942
A.Title: Complete genome sequence of Pseudomonas aeruginosa A: Larbig, K.; Lim,
Y.; Lory, S.; Olson, M.W.
Nature 406, 959-964, 2000
A.Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathc
A.Accession: G83117
A.Stetus: preliminary
A.Molecule type: DNA
A.Reference number: A82950; MUID:20437337; PMID:10984043
A.References: G8:AEO04639; GB:AEO04091; NID:g9950434; PIDN:AAGO7609.1; GSPDB:GNO01
A.Foras-references: GB:AEO04639; GB:AEO04091; NID:g9950434; PIDN:AAGO7609.1; GSPDB:GNO01
A.Foras-references: GB:AEO04639; GB:AEO04091; NID:g9950434; PIDN:AAGO7609.1; GSPDB:GNO01
A.Foras-references: GB:AEO04639; GB:AEO04091; NID:g9950434; PIDN:AAGO7609.1; GSPDB:GNO01
C.Genetics:
A.Gene: fptA; PA4221
C.Superfamily: ferric-pseudobactin receptor amino-terminal homology <TNC>
F:446-720/Domain: tonB-dependent receptor amino-terminal homology <TNC>
F:446-720/Domain: tonB-dependent receptor acrobxyl-terminal homology <TNC>
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, F.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Parrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Reference number: AB0502; PMID:11677608
A;Accession: AC0547
A;Accession: AC0547
A;Actus: preliminary
A;Residues: 1-696 <PAR>
A;Residues: 1-696 <PAR>
A;Residues: 1-696 <PAR>
A;Cross=references: GB:AL513382; PIDN:CAD08819.1; PID:g16501633; GSPDB:GN00176
C;Genetics:
A;Gene: STY0396
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BAD187

probable iron-siderophore receptor YPO1537 [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Species: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001

C;Accession: ABO187

R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
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100.0%; Pred. No. 19;
ative 0; Mismatches
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100.0%; Pred. No. 18;
iive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conservative
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A;Gene: YPO1537
C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal homo
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CAccession: Ad601; S54001; PG4227
R;Poole, K.; Neshat, S.; Krebss, K.; Heinrichs, D.E.
J. Bacteriol. 175, 4597-4604, 1993
A;Title: Cloning and nucleotide sequence analysis of the ferripyoverdine receptor gene f
A;Reference number: A40601; MUID:93328663; PMID:8335619
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUD:21470413; PMID:11586360
A;Accessaton: AB0187
A;Accessaton: Abolls7
A;Accessaton: Apolls7
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-753 <KUR>
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C;Genetics:
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Cibate: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jan-2000
Cipaccession: T30917
Sipavidson, S.; Rohlfing, T.
submitted to the EMBL Data Library, August 1999
A; Reference number: 220934
A; Reference number: 220934
A; Reterence number: 220934
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-775 cDBA
A; Residues: 1-775 cDBA
A; Residues: 1-775 cDBA
A; Residues: EMBL:AP003151; PIDN:AAB54226.2
A; Experimental source: strain Bristol N2; clone D1007
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A;Introns: 44/3; 146/3; 224/1; 343/2; 422/3; 494/3; 579/3; 668/3; 709/3
A;Note: D1007.15
C;Superfamily: Caenorhabditis elegans hypothetical protein D1007.15
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ilarity 100.0%; Pred. No. 20;
Conservative 0; Mismatches
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100.0%; Pred. No. 19;
ative 0; Mismatches
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submitted to the EMBL Data Library, March 1994
A;Referen number: S53998
A;Accession: S54000
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protein D1007.15 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
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C;Superfamily:
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A;Residues: 1-715,'Y',717-744,'YN',745-747,'S',749-813 <LAM>
A;Residues: 1-715,'Y',717-744,'YN',745-747,'S',749-813 <LAM>
R;Cross-references: EMBL:U07359; NID:g1633044; PIDN:AAB60199.1; PID:g466459
R;McMorran, B.J.; Merriman, M.E.; Rombel, I.T.; Lamont, I.L.
                                                                     A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                 R; anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
                                                                                                                                                                                                          C; Date: 10-May-2001
C; Accession: E87759
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Nature 406, 959-964, 2000
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83345
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F;184-317/Domain: tonB-dependent receptor amino-terminal homology <TNN>
F;538-813/Domain: tonB-dependent receptor carboxyl-terminal homology <T</pre>
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C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal homo
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A;Title: Characterisation of the pvdE gene which is required A;Reference number: JC5090; MUID:97075909; PMID:8918232
A;Accession: PC4227
                                                                                                                                                                                    R; anonymous,
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A;Residues: 1-49 <MCM>
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                            Status: preliminary
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8; Conser
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8; Conserv
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A.; Larbig,
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K.; Lim,
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Best Local S
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460 GLSLIGG 466
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Nakazaki, N.; Shimpo, S.; Sugimoro, P., Addition, N.; Shimpo, S.; Sugimoro, P., Addition, N.; Shimpo, S.; Sugimoro, P., Addition, Nitrogen-fixing Cyanobacterium A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Cyanobacte
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A;Residues: 1-1274 <KUR>
A;Cross-references: GB:BA000018; PID:g13701536; PIDN:BAB42830.1;
A;Experimental source: strain N315
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C; Superfamily: Caenorhabditis elegans hypothetical
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A;Molecule type: DAA
A;Residues: 1-78 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74126.1; PID:g17131519;
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada,
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: A89959
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Best Local S
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5. 21;
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Conserved hypothetical protein Atul525 [imported] - Agrobacterium tumefaciens (strain CS C)Species: Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens (Spaces: Agrobacterium tumefaciens) (Agrobacterium tumefaciens) (
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C;Date: 20-Apr-2001
C;Date: 20-Apr
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A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                              A,Cross-references: GB:AE007869; PIDN:AAK87316.1; PID:g15156613; GSPDB:GN00169
C,Genetics:
A,Gene: AGR C 2812
A,Map position: circular chromosome
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A;Molecule type: DNA
A;Redidues: 1-108 cKUR.
A;Crosd-references: GB:AE0006688; PIDN:AAL42530.1; PID:g17739951; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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100.0%; Pred. No. 42;
ative 0; Mismatches
A; Reference number: A97359; PMID:11743194
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Best Local Similarity 100.0
Matches 7; Conservative
                                               A, Accession: C97545
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-108 < KUR>
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10 AATVLAA 16
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A;Gene: ML2274
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C;Species: Chlamydia muridarum, Chlamydia trachomatis Mopn
C;Species: Chlamydia muridarum, Chlamydia trachomatis Mopn
C;Species: Chlamydia muridarum, Chlamydia trachomatis Mopn
C;Accession: C81660
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A;Recession: C81660
A;Status: preliminary
A;Accession: C81660
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-102 cfET>
A;Cross-references: GB:AE002349; GB:AE002160; NID:g7190851; PIDN:AAF39627.1; PID:g719085
A;Experimental source: strain Nigg (WoPn)
C;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: thioredoxin; thioredoxin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
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C97545
C97545
C) Propertical protein AGR C 2812 [imported] - Agrobacterium tumefaciens (strain C58, Cere C) Properterical protein AGR C 2812 [imported] - Agrobacterium tumefaciens
C) Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C; Accession: C97545
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
                                                                                                                                                                                                                                                                                                   C;Species: Nostoc sp. A;Note: Nostoc sp. A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 5.0 bate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AC1886 R;Raneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.;
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A;Molecule type: DNA
A;Residues: 1-84 «KUR»
A;Cross-references: GB:BA000019; PIDN:BAB72594.1; PID:g17129982; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Genetics:
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26 GLSLIGG
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Gaps

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A; Duction France: DNA
A; Molecule type: DNA
A; Residues: 1-127 < OLI>
A; Cross-references: EMBL: Z99296; PIDN: CAB16594.1; GSPDB: GN00066; SPDB: SPAC3H5.10
A; Cross-references: EMBL: Z99296; PIDN: CAB16594.1; GSPDB: GN00066; SPDB: SPAC3H5.10
A; Cross-references: EMBL: Z99296; PIDN: CAB16594.1; GSPDB: GN00066; SPDB: SPAC3H5.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60s ribosomal protein L32 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
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A;Residues: 1-123 <STO>
A;Cross-references: GB:AE004919; GB:AE004091; NID:g9951346; PIDN:AAG08440.1; GSPDB:GN001
A;Experimental source: strain PAO1
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A;Residues: 1-123 <TIM
A;Residues: 1-123 <TIM
A;Residues: 1-123 <TIM
A;Cross-references: EMBL:X66592; NID:g45388; PIDN:CAA47150.1; PID:g45390
A;Cross-references: EMBL:X66592; NID:g45390
A;Cross-refer
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Best Local Similarity
Thes 7; Conserve
                                                                                                                                                                                A; Map position:
C; Superfamily:
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A; Accession: T38756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Reference number: A82950; MUID:20437337; PMID:10984043
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A;Title: Cloning and molecular analysis of the poly(3-hydroxyalkanoic acid) gene locus
A;Reference number: S29303; MUID:93011120; PMID:1396693
A;Accession: S29304
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C;Species: Pseudomonas aeruginosa
C;Date: 10-Mar-1994 #sequence revision 10-Mar-1994 #text_change 31-Dec-2000
C;Accession: S29304; B83013; S28376
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                                                                                                                                                                                                                                                           A; Gene: SPDB:SPAC3H5.10
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                                                                   100.0%;
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100.0%; Pred. No. 47,
ive 0; Mismatches
                                                               1.0%; Score 7; 1
100.0%; Pred. No.
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o. 47;
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o. 43;
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A.; Larbig, K.; Lim,
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                                 R;Grellet, F.; Cooke, R.; Laudie, M.; Raynal, M.; Delseny, M. submitted to the EMBL Data Library, October 1995 A;Reference number: S71253 A;Recession: S71256
                                                                                                                                                                                                       ribosomal protein L27a, cytosolic - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text
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                                                                                                                                                                         C; Accession: S71256
A;Molecule type: mRNA
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A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-127 <PUR>
                                                                                                                                                                                A; Gene: BH3761
                                                                                                                                                                                                                          A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07480.1; GSPDB:GN00 A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                        A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A84120
                                                                                                                                                                                                                                                                                                                                                                                   R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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C;Superfamily: rat ribosomal protein L32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Purnelle, B.; Goffeau, A.; Wood, V.; Lyne, M.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, February 1998
A;Reference number: Z21863
A;Accession: T39562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP synthase protein BH3761 [imported] - Bacillus halodurans (strain C-125)
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Matches
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                                          632 NLWTTYO 638
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                                                                                Local Similarity nes 7; Conserv
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47 NLWITYO 53
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b; Pred. No. 48;
0; Mismatches
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                                                                                                           Score 7; ; Pred. No.
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#text_change

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RESULT 30
877384
hypothetical protein sll1455 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: 877384
R;Kaneko, T:; Sato, S:; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Owmura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA, Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:D90906; GB:AB001339; NID:g1652492; PIDN:BAA17487.1; PID:g165256.
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein sll1455
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A.Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A; Reference number: AD3252; PMID:11756688
A;Cross-references: EMBL:Z72625; NID:g1322642; PIDN:CAA96808.1; PID:g1322643; GSPDB:GN00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable competence-damage protein [imported] - Brucella melitensis (strain 16M)
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A;Molecule type: DNA
A;Residues: 1-165 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52043.1; PID:g17982810; GSPDB:GN00190
A;Experimental source: strain 16M
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                            AjExperimental source: strain $288C
CjGenetics:
AjGene: SGD:CYH2; RPL29; MIPS:YGL103w
AjCross-references: SGD:S0003071; MIPS:YGL103w
Ajrup position: 7L
Ajintrons: 17/1
CjSuperfamily: rat ribosomal protein L27a
CjSuperfamily: rat ribosomal protein L27a
Fj2-149/Product: ribosomal protein L27a.e #status experimental <MAT>
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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larity 100.0%; Pred. No. 57;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             Length 149
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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100.0%; Pred. No. 55;
tive 0; Mismatches
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Matches 7; Conservative
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Best Local Similarity
T; Conserve
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REBY29

Tibosomal protein L27a.e, cytosolic - yeast (Saccharomyces cerevisiae)

NiAlternate names: protein G3101, protein YGL103w; ribosomal protein YL29

C;Species: Saccharomyces cerevisiae

C;Date: 25-Feb-1985 #sequence_revisiae

C;Accession: A07782; S4569; S64110

R;Kacufer, N.F.; Fried, H.M.; Schwindinger, W.F.; Jasin, M.; Warner, J.R.

A;Title: Cycloheximide resistance in yeast: the gene and its protein.

A;Accession: A02782

A;Molecule Lype: DNA

A;Residues: 1-149 KAU-

A;Title: Transcriptional elements of the yeast ribosomal protein gene CYH2.

A;Title: Transcriptional elements of the yeast ribosomal protein gene CYH2.

A;Title: Transcriptional elements of the yeast ribosomal protein gene CYH2.

A;Title: Transcriptional elements of the yeast ribosomal protein gene CYH2.

A;Title: Transcriptional elements of the yeast ribosomal brotein gene CYH2.

A;Title: Transcriptional elements of the yeast ribosomal some subsiders: 1-16 kGCM.

A;Reference number: S45696

A;Molecule Lype: DNA

A;Reference number: S45696

A;Molecule Type: DNA

A;Reference number: S64101

A;Molecule type: DNA

A;Reference number: S64101

A;Molecule type: DNA

A;Residues: 1-149 kRE>
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Cryspecies: Lactococcus lactis subsp. lactis
Cryspecies: Cs6732
Cryspecies: Cs6732
A; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A; Reference number: A86625; MUID:21235186; PMID:11337471
A; Residues preliminary
A; Molecule type: DNA
A; Residues: 1-148 «STO»
A; Cross-references: GB:AE005176; PID:g12723787; PIDN:AAK04957.1; GSPDB:GN00146
A; Experimental source: strain IL1403
C; Genetics:
A; Gene: ahrC
C; Superfamily: Escherichia coli arginine repressor argR
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                            A;Cross-references: EMBL:X91959; NID:g1107486; PIDN:CAA63025.1; PID:g1107487 C;Superfamily: rat ribosomal protein L27a C;Keywords: protein biosynthesis; ribosome
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1.0%; Score 7; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                 Length 146;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                 1.0%; Score 7; DB 2;
100.0%; Pred. No. 54;
tive 0; Mismatches
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Best Local Similarity 100.(
Matches 7; Conservative
A;Residues: 1-146 <GRE>
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DB 2;

Score 7;

1.0%;

Query Match

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C;Accession: C86231
R;Theologis, A.; Ecker, J.R.; Palm, Chin, C.W.; Chung, M.K.; Conn, L.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; I Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyla pseudotsugata multinucleocapsid A;Reference number: Z17011; MUID:97271300; PMID:9128251
A;Accession: T10313
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                                                                                            hypothetical protein [imported] - Arabidopsis tha C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, Lory, S.; Olson, M.V.
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A; Residues: 1-173 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein PA4661 [imported] - Pseudomonas aeruginosa (strain PAO1)
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Pseudomonas aeruginosa
Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                 Experimental source: strain PAO1
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7; Conserv
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                                                                                          #sequence_revision
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Pred. No.
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                                Conway,
                                    C.J.; Federspiel, N.A.;
Conway, A.B.; Conway, A.
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                        02-Mar-2001 #text_change 31-Mar-2001
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                                  iel, N.A.; Kaul, S.; White, O.; Conway, A.R.; Creasy, T.H.; Dev
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A.; Larbig,
                                                                                                                                                                                                                                                                                                   Gaps
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K.; Lim,
                                    Alonso, war, K.;
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-174 <STO>
                                                                                                                            A; Map position: 1
                                                                                                                                                  A;Cross-references: GB:AE005172; NID:g2160182; PIDN:AAB60745.1; GSPDB:GN00141
C;Genetics:
                                          Matches
                                                            Query Match
Best Local
200 DVSGSLN 206
                                     Local Similarity nes 7; Conser
                                          Conservative
                                                            1.0%;
                                          0
                                                            Score 7;
Pred. No.
                                            Mismatches
                                                            DB 2
                                          0
                                                                                  Length
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                                          Indels
                                          <u>,</u>
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Maiti, R.; Ma
                                        Gaps
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N;Alternate names: hydrogen ion-transporting ATPase delta chain C;Species: Escherichia coli C;Date: 18-Dec-1981 #sequence_revision 02-Apr-1982 #text_change C;Accession: A93732; A90101; I41274; H65176; T45005; A01031 R;Gay, N.J.; Walker, J.E. R;Gay, N.J.; Walker, J.E. Nucleic Acids Res. 9, 3919-3926, 1981 H+-transporting two-sector ATPase (EC 3.6.3.14) delta chain - E N;Alternate names: hydrogen ion-transporting ATPase delta chain Escherichia coli (strain 01-Mar-2002

A;Title: The atp operon: nucleotide sequence of the promoter A;Reference number: A93732; MUID:82059437; PMID:6272190 A;Accession: A93732 A; Molecule type: DNA A; Residues: 1-177 <GAY> and the genes for the membr

A; Cross-references: GB: V00264; GB: X00771; NID: g41023; PIDN: CAA23517.1;

PID:g41028

R;Mabuchi, K.; Kanazawa, H.; Kayano, T.; Futai, M. Biochem. Biophys. Res. Commun. 102, 172-179, 1981 A;Title: Nucleotide sequence of the gene coding for the A;Reference number: A90101; MUID:82068433; PMID:6458296 A;Accession: A90101 delta subunit of

A;Molecule type: DNA A;Residues: 1-81,'D',83-177 <MAB> A;Residues: 1-81,'D',83-177 <MAB> ` ~~~~~references: GB:M12212; GB:M12213; NID:g145396; PIDN:AAA20044.1; PID:g145398

R;Kanazawa, H.; Futai, M.
Ann. N. Y. Acad. Sci. 402, 45-64, 1982
A;Title: Structure and function of H+-ATPase: What we ha A;Reference number: I41271; MUID:83176724; PMID:6301339
A;Accession: I41274
A;Accession: I41274 have learned from Escherichia

A;Status: preliminary; translated from A;Molecule type: DNA GB/EMBL/DDBJ

A; Residues: 1-177 < RES>

A;Cross-references: GB:M25464; NID:g146318; PIDN:AAA83872.1; PID:g146322 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.A.; Rose, D.J.; Mau, B.; Shao, Y. V.; Riley,

Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H65176

K-12

A; Status: preliminary; nucleic acid sequence not shown; translation not

A; Molecule type: DNA A; Residues: 1-177 <BLAT>

PIDN:AAC76758.1; PID:g1790173;

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A;Cross-references: GB:AE000450; GB:U00096; NID:g1790166; A;Experimental source: strain K-12, substrain MG1655 R;Nielsen, J.; Hansen, F.G.; Hoppe, J.; Friedl, P.; Von Me Mol. Gen. Genet. 184, 33-39, 1981 A;Title: The nucleotide sequence of the atp genes coding f A;Reference number: ZZ2893; MUID:82147764; PMID:6278247 A;Accession: T45005

A;Status: preliminary; translated from GB/EMBL/DDBJ

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H+-transporting two-sector ATPase (EC 3.6.3.14) delta chain [imported] - Yersinia pestis C; Species: Yersinia pestis C; Shacession: AH0500 R; Prentice, M.B., Spackhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. Rachon-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, M. A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A; Reference number: AB0001; MUID:21470413; PMID:11586360
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Jun-2002
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A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome A.Reference number: A99629; MUID:21156231; PMID:11258796
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hypothetical protein VCA0195 [imported] – Vibrio cholerae (strain N16961 serogroup O1)
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A,Molecule type: DNA
A,Residues: 1-177 <HAY>
A,Cross-references: GB:BA000007; PIDN:BAB38100.1; PID:gl3364152; GSPDB:GN00154
A,Experimental source: strain O157:H7, substrain RIMD 0509952
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C;Superfamily: H+-transporting ATP synthase delta chain
C;Keywords: hydrolase
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C;Superfamily: H+-transporting ATP synthase delta chain
C;Keywords: hydrolase
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1.0%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches
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100.0%; Pred. No. 64;
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A; Residues: 1-177 < KUR>
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F86059
H+transporting two-sector ArPase delta chain [similarity] - Escherichia coli (strain O15 C; Species: Escherichia coli
C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C; Accession: F86059
R; Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: F86059
A; Cession: F86059
A; Cession: F86059
A; Residues: 1-177 <STO>
A; Residues: 1-177 <STO>
A; Residues: 1-177 <STO>
A; Residues: 1-177 <STO>
A; Cygenteics: C; Genetics:
A; Genetic
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Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 17-May-2002

C;Accession: AC0954

R;Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S; Moule, S; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova

A;Reference number: AB0502; PMID:11677608

A;Ressious: AC0954

A;Ressious: Preliminary

A;Molecule type: DNA

A;Ressidues: 1-177 <PAR>

A;Cosession: AC0954

A;Cosession: AC0954

A;Cosession: AC0954

A;Genetics:

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A;Genetics:

A;Genetics:

A;Genetics:
                                                   A; Residues: 1-177 < NIE>
A; Ross-treferences: EMBL:V00266; NID:g41031; PIDN:CAA23524.1; PID:g41034
A; Cross-treferences: EMBL:V00266; NID:g41031; PIDN:CAA23524.1; PID:g41034
C; Genetics: atpH; uncH
A; Map position: 84 min
C; Complex: this is one of the five chains of the enzymatic component (F1) of the ATPase C; Superfamily: H++transporting ATP synthase delta chain
C; Reywords: ATP biosynthesis; hydrolase; membrane-associated complex
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Similarity 100.0%; Pred. No. 64;
7; Conservative 0; Mismatches
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Best Local Similarity
Matches 7; Conserv
                         A; Molecule type: DNA
A; Residues: 1-177 <NIE>
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R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapp nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morri A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 4
A;Introns: 53/3; 80/3
A;Note: F17A8.180
C;Superfamily: Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F17A8.180 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Sep-1999
A;Reference number: A95000;
A;Accession: E95072
A;Status: preliminary
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A; Accession: T04031
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A;Accession: D82490
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Nature 406, 477-483, 2000
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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R;Tettelin, H.; Nelson,
                                                                                                                                                                                                          C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
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A;Experimental source: cultivar Columbia;
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A; Residues: 1-191 <BEV>
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A; Residues: 1-182 <HEI>
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                                                                                                                                                                                                                                                            nitroreductase family protein [imported] - Streptococcus
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01; strain N16961; biotype El Tor
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Radune, D.; Holtzapple,
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-208 <STO>
A;Cross-references: GB:AE005176; PID:g12725039; PIDN:AAK06092.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
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A;Cross-references: GB:AE005672; PIDN:AAK74774.1; PID:g14972098; GSPDB:GN00164; TIGR:SP4.
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0622
                                                                                                                                                         A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: B86874
                                                                                                                                                                                                   R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                              hypothetical protein yuhE [imported] - Lactococcus lactis subsp. lactis (strain C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: B86874
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C;Keywords:
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IGGGVNA 651

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RESULT 45
AG2841
outer membrane protein omp [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AG2841
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
S;Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AG2841
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-209 *kUR>
A;Cross-references: GB:AE008688; PIDN:AAL43149.1; PID:g17740625; GSPDB:GN00186
C;Genetics
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1.0%; Score 7; DB 2; Length 209;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels
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Search completed: December 18, 2002, 06:59:29 Job time: 40.351 secs

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Minimum DB
Maximum DB
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is derived by analysis of the total score distribution.
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  GenCore version (c) 1993 - 2002
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ICPO_HSVEB
LEU1_MYCTU
FOXA_SALTY
FPTA_PSEAE
FPVA_PSEAE
THIO_CHLMU
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ET3_MOUSE
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RL34 RICPR
RL34 RICPR
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RL31 ECOLI
YEBD ECOLI
YEBD ECOLI
YOKZ CAEBL
YED HAEIN
YOKZ CAEBL
YED HAEIN
YOHV BACSU
YOHU BACSU
MGF RABIT
MIRZ HUMAN
MIRZ HUMAN
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H4 EÜPCR
MIRZ RAT
YDZF BACSU
CSGC_ECOLI
Y518 METTH
Y655_BACHD
RNPA_PASMU
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HRP3_SCHPO
YD34_YEAST
RRPO_NMV
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EF2 BLAHO
DLG1 DROME
UBP4 HUMAN
REV1 YEAST
NME3 MOUSE
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HAP4 YEAST
C791 SORBI
C09 ONCMY
C09 FUGRU
YKG5 CAEEL
PSO2 YEAST
RED1 RAT
YJL2 YEAST
HEPA HSVEB
RED1 HUMAN
GUND CELFI
Y363 METJA
RHP9 SCHPO
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VGLG_HSVEB
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Included Acids Res. 284.317-4331 (2000).

Included Selection Condensation reaction between C acroms 2 and 3 of pyruvate and glyceraldebyde 3-phosphate to yield 1-deoxy-D-xylulose-5-phosphate (DXP) (By similarity).

Included AcTIVITY: Pyruvate + D-glyceraldebyde 3-phosphate = 1-deoxy-D-xylulose 5-phosphate + CO(2).

COFACTOR: Thiamine pyrophosphate (By similarity).

Included Selection Cofficient C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBŪNIT: Homodimer (By similarity).
SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY. DXS SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                 P40482
Q9bn24
Q95109
P98198
P7563
P23159
P57996
P95759
Q12220
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P71494
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16-OCT-2001 (Rel. 40, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 4.1.3.37) (1-deoxy-Bazzy)
DXS OR BH2779
Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    629 AA
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AACT_DROME
SC24_YEAST
SYA_HALN1
SECA_SYNY3
A8B2_HUMAN
                                                                     A8BZ_HUMAN
V321_MYCGE
ODOI_BACSU
SEA1_MYCLE
SECA_STRGR
DIP2_YEAST
ABB3_HUMAN
C1TC_YEAST
SECA_STRCO
PPMAS_ARATH
SECA_STRCO
SECA_STRCO
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InterPro; IPR00360; Transketolase.
Pfam; PF02779; transket.pvr; 1.
Pfam; PF02779; transketolase_c; 1.
TIGRFAMs; TIGRO0204; dxs; 1.
PROSTIE: PS00801; TRANSKETOLASE_1; 1.
PROSITE; PS00802; TRANSKETOLASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
                                    STANDARD;
                 00000000000000000
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Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DXS_BACHD
Q9K971;
16-OCT-2001 (
16-OCT-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21145866; PubMed=11248100; May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                                                                                                                                                                           Gaps
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Pasteurella.
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Lyase; Flavoprotein; Thiamine pyrophosphate;
Isoprene biosynthesis; Thiamine biosynthesis; Complete
SEQUENCE 629 AA; 69279 MW; 7B5909B2F427CIIE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAA9F9C64442C7BB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- COFACTOR: MANGANESE (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE RNASE HII FAMILY.
                                                                                                                    DB 1;
. 0.79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ribonuclease HII (EC 3.1.26.4) (RNase HII).
RNHB OR PM1998.
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                                                                                                                 1.2%; Score 9; I
100.0%; Pred. No.
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Pred. No.
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HSSP; Q57599; 1EKE.
INLECTPO; IPRO01352; RNase HII/HIII.
PÉan; PPO1351; RNase HII/III.
HYdrolase; Nuclease; Endonuclease; Ma
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299 GHYKIESGE 307
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ICPO_HSVEB
ID _ICPO_H
AC P28990
DT 01-DEC
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RNH2_PASMU
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-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-!- SIMILARITY: TO OTHER HERPESVIRUSES ICPO PROTEIN.
                                                                                                                                                 TURN
HELIX
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Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR OF 1-63.
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J. Mol. Biol
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Viruses; dsDNA viruses, no RNA sta
Alphaherpesvirinae; Varicellovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      novel arrangement of zinc-binding; the C3HC4 motif of an alpha herpes Mol. Biol. 234:1038-1047(1993).
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A sequence of equine herpesvirus-1.
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PS50089; ZF_RING_2; 1.
ption regulation; Trans-acting
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718; PubMed=8263911;
Barlow P.N., Milner
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P96420; C66677;
30-MAY-2000 (Rel. 3
30-MAY-2000 (Rel. 3
15-JUN-2002 (Rel. 4
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KEDLINE=98295987; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Rogers J., Stelton S., Squares S., Squares R., Rogers J., Stelton S., Squares S., Squares R., Rogers J., Rogers J., Stelton S., Squares S., Squares R., Rogers J., Rogers J., Stelton S., Squares S., Squares R., Rogers J., Rog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rutter S., Seeger K., Skelton S., Squares S., Squares F. Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis complete genome sequence.";
Nature 393:537-544(1998).
                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (APR-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CDC 1551 / Oshkosh; Fleischmann R.D., Alland D
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
2-isopropylmalate synthase (EC 4.1.3.12) (Alpha-isopropylmalate synthase) (Alpha-IPM synthetase).
LEUA OR RV3710 OR MT3813 OR MTV025.058.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Catalyzes the condensation of the acetyl group of acetyl-CoA with 3-methyl-2-oxobutanoate (2-oxobisovalerate) to for 3-carboxy-3-hydroxy-4-methylpentanoate (2-isopropylmalate).

CATALYTIC ACTIVITY: 3-carboxy-3-hydroxy-4-methylpentanoate + CoA acetyl-CoA + 3-methyl-2-oxobutanoate + H(2)0.
                                                                                                                                                                                                                                                       in positions 49 and 77.
                                                                                                                                                                                                                                                                                      CAUTION: Ref.1 sequence differs from that shown due to
                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE ALPHA-IPM SYNTHETASE SYNTHASE FAMILY. LEUA 2 SUBFAMILY.
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tuberculosis alpha-isopropyl malate
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702 AA;
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16-OCT-2001
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MEDLINE=95370139; PubMed=7642488;
MEDLINE=95370139; PubMed=7642488;
MEDLINE=95370139; PubMed=7642488;
Tsolis R.M., Baumler A.J., Stojiljkovic I., Heffron F.;
Tsolis R.M., Baumler A.J., Stojiljkovic I., Heffron P.;
regulated genes.,
J. Batchiol of Salmonella typhimurium: identification of new iron-regulated genes.,
J. Batchiol of Reservation of New Proymer, IN ASSOCIATION WITH THE TONB PROYEIN (BY SIMILARITY). MAY PLAY A ROLE IN INTESTINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=LTZ / SGSC1112 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
COUTENDY L., PORWOLLIK S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=SL1344,
BDDLINE39203118; PubMed=10103258;
Kingsley R.A., Reisbrodt R., Rabsch W., Ketley J.M., Tsolis R.M.,
Kingsley R.A., Bougan G., Baeumler A.J., Roberts M., Williams P.H.;
Everest P., Dougan G., Baeumler A.J., Roberts M., Williams P.H.;
"Ferrioxamine-mediated iron(III) utilization by Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
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                                                                                                                                                                                                                                        533 TTASLR -> NRPA (IN REF. 1).
544 AAR -> RHARTALN (IN REF. 1).
70113 MW; 881A9AAEA7F8FB71 CRC64;
                                                                                                                                                                                                                                                                                                                  Length 644;
                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                     Tuberculist; Rv3710; -...Tuberculist; Rv3710; -...Tuberculist; Rv3710; -...Tuberpro; IPR002034; AIPM/Hcit_synth.
InterPro; IPR000891; HMGL-like.
Ffan, PF00682; HMGL-like; 1.
TIGREAMS; TIGR00970; leuA, yeast; 1.
PROSITE; PS00815; AIPM_HOWOCIT_SYNTH_1; 1.
PROSITE; PS00816; AIPM_HOWOCIT_SYNTH_2; 1.
Leucine biosynthesis; Lyase; Complete proteome.
                                                                                                                                                                                                                                                                                                                  1.1%; Score 8; DB 1;
100.0%; Pred. No. 8.8;
tive 0; Mismatches
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ferrioxamine B receptor precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appl. Environ. Microbiol. 65:1610-1618(1999).
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AL022121; CAA18032.1; -. AE007178; AAK48181.1; ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                 644 AA;
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                                           MT3813;
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Q56145;
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                    EMBL;
TIGR;
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Matches
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  DR REAL PROPERTY OF THE SOLUTION OF THE SOLUTI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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C. STRAIN-ATCC 156-92 / PAO1;

MEDLINE-20437337; PubMed=10984043;

MEDLINE-20437337; PubMed=10984043;

Stover C. K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

A Garber R.L., Goltry L., Tolentino E., Westbrock-Wedman S., Yuan Y.,

A Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

A Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

I opportunistic pathogen.";

I nature 466:595-964(2000).

I nature 466:595-964(2000).
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BEDILNES-PA117363; PubMed-8288523;
Ankenbauer R.G., Quan H.N.;
"FptA, the Fe(III)-pyochelin receptor of Pseudomonas aeruginosa: a
                                                                                                                                                                                                                                                            EMBL; AE008712; AAL19318.1; -.
EMBL; AF060876; AAC15464.1; -.
EMBL; AF060876; AAC15464.1; -.
HSSP; P06971; 1BY5.
StyGene; SG10646; foxA.
InterPro; IPR000531; TonB boxC.
PROSITE; PS00430; TONB DEPENDENT REC_1; FALSE_NEG.
PROSITE; PS01156; TONB DEPENDENT REC_2; FALSE_NEG.
Signal; Receptor; Transmembrane; Outer membrane; Iron transport;
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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249 MAYP - S SPYL (IN REF. 2).
275 G -> R (IN REF. 2).
279 F -> S (IN REF. 2).
352 A -> P (IN REF. 2).
373 HALLVGI -> SSSAGGD (IN REF. 7).
77685 MW, 7E2CB405B09B860D CRC64;
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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Pred. No.
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FPTA OR PA4221.
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100.0%; Pred
0; M
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Best Local S
Matches 8
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                "Complete genome sequence of Pseudomonas aeruginosa opportunistic pathogen.";
Nature 406:959-964(2000).
                                                        MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.,
                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=ATCC 15692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ferripyoverdine receptor precursor. FPVA OR PA2398.
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Pfam; PF00593; TonB_boxC; 1.
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                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                   STRAIN=PAO;
                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93328663; PubMed=8335619;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                             Poole K., Neshat S., Krebes K., Heinrichs D.E.; "Cloning and nucleotide sequence analysis of the receptor gene fpvA of Pseudomonas aeruginosa."; J. Bacteriol. 175:4597-4604(1993).
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
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TE; PS01156; TONB_DEPENDENT_REC_2; 1.
membrane; Iron transport; Transport; Signal; Receptor;
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8; Conserv
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 RECEPTOR
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720 F
720 T
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 FOR
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THE SIDEROPHORE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Pred. No.
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 FERRIPYOVERDINE
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Best Local :
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MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R.,
White O., Hickey E.K., Peterson J., Utterback
Linher K., Weidman J., Khouri H., Craven B.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., Mc
Eisen J., Fraser C.M.;
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis Mo
pneumoniae AR39.";
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SIGNAL
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Pfam; PF00593; TonB_boxC; 1.

PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.

PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.

Outer membrane; Iron transport; Transport; TonB_box; Signal; Receptor;
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EMBL; U07359; AAB60199.1; -.
EMBL; AE004666; AAG05786.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                   Nucleic Acids Res. 28:1397-1406(2000).

-- FUNCTION: participates in various redox reactions through the reversible oxidation of its active center dithiol to a disulfide and catalyzes dithiol-disulfide exchange reactions.
                                                                                                                                                                                                                                                                                                       Chlamydia muridarum.
Bacteria; Chlamydiales;
                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                           Q9РJK3;
16-ОСТ-2001
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                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       NCBI_TaxID=83560;
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INDUCTION: BY THE SIDEROPHORE, PYOVERDINE, AND UNDER STARVATION CONDITIONS.
SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR P SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR P CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-16 IS
                                                      and catalyzes dithiol-disulfide exchange react SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
 European
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                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.18;
                                                                                                                                                                                                                                                                                                        Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 8; 1; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TONB C-TERMINAL Y -> F (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FERRIPYOVERDINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> R (IN REF. 1)
A11AE4AA5A290F35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                     Gill S.R., Heidelberg J.F.,
., Utterback T., Berry K., Bass S.,
Craven B., Bowman C., Dodson R.,
lonay J., McClarty G., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                         102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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ng as its content is in no
 There
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                                                                                                                                           MoPn
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s and the
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                                                                                                                                           and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels .
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restrictions
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                           a collaboration
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               outstation
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 on
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Mood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A., Squros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Books K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., A James K., Jones L., Jones M., Leather S., McDonald S., Nagles R., James K., Jones L., Jones L., Mungall K., Murphy L., Niblett D., Odell C., Andrew R., Oliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E., Antherford K., Rutter S., Saunders B., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Welton J., Simmonds M., Squares R., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Antichen I., Vanstreals E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Andibert B., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Galllardin C., Mancron J., Sanchez M., Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Dominguez A., Revuelta J.L., Moreno S., Ammstrong J., Foreburg S.L., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Shakavovski G.V., Ussery D., Barrell B.G., Nurse P., Narwer G., Lenger D., Sanchez M., Schaek B., Narwer D., Sanchez M., Shakavovski G.V., Ussery D., Barrell B.G., Nurse P., Narwer G., Lenger D., Sanchez M., Shakavovski G.V., Wastrell D., Narwer D., Sanchez M., Shakavovski G.V., Wastrell B.G., Nurse P., Shakavovski G.V., Wastrell B.G., Nurse P., Shakavovski G.V., Sanchez M., Shakavovski G.V., Sanchez M., Shakavovski G.V., Wastrell B.G., Nurse P., Shakavovski G.V., Sanchez M., Shakavovski G.V., Sanchez M., Shakavovski G.V., Sanchez M., Shakavovski G.V., Sanchez M., Salaskovski G.V., San
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
                                                                                                                                                                      TIGR; TC0826; -
InterPro; IRR00063; Thiored.
Pfam; PF00085; Linored; 1.
PRINTS; PR00421; THIOREDOXIN.
TIGRAMS; TIGR01068; thioredoxin; 1.
PROSITE; PS00194; THIOREDOXIN; 1.
Redox-active center; Electron transport; Complete proteome.
DISULFID 28 31 REDOX-ACTIVE (BY SIMIARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
15-DBC-1998 (Rel. 37, Last sequence update)
15-UDC-2002 (Rel. 41, Last annotation update)
62 ribosomal protein L32-A.
RPL32A OR SPAC3HS.10.
                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Score 7; DB 1
100.0%; Pred. No. 20;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21848401; PubMed=11859360;
                                                                                                                          EMBL; AE002349; AAF39627.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces.
NCBI TaxID=4896;
                                                                                                                                                   P80579; 1QUW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 ASPRPAE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 ASPRPAE 63
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDIANUS 21844401; PubMed=11859360;

Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Squored V., Gwilliam R., Hardan D., Basham D., Boward S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Rochies S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgoon G.,

And Holroyd S., Horneby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

And Holroyd S., Monles M., Leather S., McDonald S., McLean J.,

Mooney P., Moule S., Mungall K., Murbhy L., Niblett D., Odell C.,

And Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Rutherford K., Taylor R.G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Berzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Berzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Borzym K., Cruzado L., Jimenez S., Gloux S., Lelaure V., Mottler S.,

Ceffeau A., Cadleu E., Dreane S., Gloux S., Lelaure V., Mottler S.,

Boninguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

Cerruttil L., Lowe T., McCombie W.R., Paulsen I., Potcashkin J.,

Ryder L., Lowe T., Wccombie W.R., Paulsen I., Potcashkin J.,

Ryder R., R., Paulsen I., Berky D., Barrell B.G., Nurse P.,

Ryder R., Shapakovski G.V., Ussery D., Barrell B.G., Nurse P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- MISCELLANEOUS: THERE ARE TWO GENES FOR L32 IN S.POMBE.
-!- SIMILARITY: BELONGS TO THE L32E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 AA; 14458 MW; 4BBB3CEB2E359E05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.0%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
60S ribosomal protein L32-B.
60S ribosomal protein L32-B.
8chizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB000914; BAA19212.1; -.
InterPro; IPR001515; Ribosomal_L32E.
Probom; PD003823; Ribosomal_L32e; 1.
Probom; PD003823; Ribosomal_L32E; 1.
PROSTTE; PS00580; RIBOSOMAL_L32E; 1.
Ribosomal protein; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z99296; CAB16594.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
RR3B SCHPO
AC 042935;
DT 15-DEC-1998
DT 1
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ID COBDT 16-OC
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Best Local S
Matches 7
Best Local Similarity
Matches 7; Conserv
                                                       Query Match
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16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Priess H., Brauer B., Schmidt C., Kamp D.;
Priess H., Brauer B., Schmidt C., Kamp D.;
"Sequence of the left end of Mu.";
"Sequence of the left end of Mu.";
(In) Symonds N., Toussaint A., van de Putte P., Howe M.M.
(In) Symonds N., Toussaint A., van de Putte P., Howe M.M.
(In) Symonds N., Toussaint A., van de Putte P., Howe M.M.
                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EWBL outest the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Morgan G., Hatfull G., Hendrix R.;
"Genome of bacteriophage Mu and comparison with the Haemophilus influenzae Mu-like prophage FluMu,";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                           SEQUENCE
                                                                                                                                    Hypothetical
                                                                                                                                                        EMBL; M64097; AAA32391.1; -. EMBL; AF083977; AAF01134.1; -.
                                                                                                                                                                                                                                     entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, Mu-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribosomal protein;
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ProDom; PD003823; Ribosomal_L32E; 1.
PROSITE; P800580; RIBOSOMAL_L32E; PALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage
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                                                                                                         il protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
Ма
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ein; Multigene family
AA; 14445 MW; 01490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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LONGS TO THE 132E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                         16310 MW;
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                           100.0%;
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                        1.0%; Score 7; 1
100.0%; Pred. No.
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  0;
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                                                                                                         80ACAC9B18F10A93 CRC64;
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  Mismatches
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o. 24;
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RX Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA Theologis A., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Dunn F., Etgu P., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-cv. Columbia; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced "SSP consortium (Salk/Stanford/PGEC).";
                                                                     EMBL; AC005292; AAF86998.1; --
EMBL; AF349525; AAK15572.1; --
EMBL; AF34716; AAG40067.1; --
EMBL; AF410280; AAK95266.1; --
EMBL; Z26208; CAA81190.1; --
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eddicotyledons; core evenosids II; Brassicales; Brassicaceae; Arabidopsis.
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15-JUN-2002 (Rel. 41, Last annotation update)
60S ribosomal protein L27a-B.
RPL27AB OR ATIG23290 OR F26F24.13 OR F26F24_23.
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          InterPro; IPR001196; Ribosomal_L15.
Pfam; PF00256; L15; 1
PROSITE; PS00475; RIBOSOMAL_L15; FALSE_NEG.
                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1993) to -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 3-141 FROM N.A.
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TO THE L15P FAMILY OF RIBOSOMAL PROTEINS
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RL28_YEAST
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SEQUENCE TO Columbia;

XTAIN=CV. Columbia;

XTAIN=CV. Columbia;

XTAIN=CV. Columbia;

XTAIN=COLUMBIA:

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15-JUN-2002 (Rel. 41, Last annotation update)
60S ribosomal protein L27a-C.
RPL27AC OR ATIG70600 OR F24J13.17 OR F5A18.22.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-cv. Columbia;
MEDLINE=97336304; PubMed=9193080;
Cooke R., Raynal M., Laudie M., Delseny M.;
"Identification of members of gene families in Arabidopsis thaliana by contig construction from partial cDNA sequences: 106 genes encoding 50 cytoplasmic ribosomal proteins.";
Plant J. 11:1127-1140(1997).
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                                                                                                                                        DB 1; Length 146; 27;
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3 4 TA -> DG (IN REF. 3).
31 G -> V (IN REF. 3).
139 I G -> C (IN REF. 3).
146 AA; 16292 MW; OCAGCO19D8BIA565 CRC64;
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Pred. No.
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RESULT 13

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Underwood M.R., Fried H.M.;
"Characterization of nuclear localizing sequences derived from yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-89220732; PubMed=6304624;
MEDLINE-89220732; PubMed=6304624;
Kaufer N.F., Fried H.M., Schwindinger W.F., Jasin M., Warner J.R.;
"Cycloheximide resistenance in yeast: the gene and its protein.";
Nucleic Acids Res. 11:3123-3135(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 17, Last annotation update)
60S ribosomal protein L28 (L27A) (L29) (YL24) (RP62).
RPL28 OR CYH2 OR YGL103W
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycescales; Saccharomycetales;
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100.0%; Pred. No. 27;
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PROSITE; PS00475; RIBOSOMAL_LIS; FALSE_NEG
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send an email to license@isb-sib.ch)
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                                                                            EMBL; AC011663; AAG52338'1; -.
EMBL; Z17767; CAA79059.1; -.
InterPro; IPR001196; Ribosomal_L15.
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                                                EMBL; X91959; CAA63025.1;
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EMBO J. 9:91-99(1990).
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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tes 7; Conserv
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SEQUENCE FROM N.A.
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54 GKVGMRY 60
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PROSITE; PS00475; RIBOSOMAL L15; 1.

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010299;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
60S ribosomal protein L27a (L29).
Erysiphe graminis (subsp. hordei) (Grass mildew).
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales, Erysiphaceae; Blumeria.
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InterPro; IPR001196; Ribosomal_L15.
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY; BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erysiphales; Erys
NCBI_TaxID=62688;
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01-NOV-1997
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PIR; A02782; R6BY29
SGD; S0003071; RPL2
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149 AA;
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RESULT 17
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SEQUENCE FROM N.A.

MEDLINE=82147764; PubMed=6278247;

Nielsen J., Hansen F.G., Hoppe J., Friedl P., von

"The nuclectide sequence of the atp genes coding
a, b, c and the F1 subunit delta of the membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=85121806; PubMed=6395859;

Walker J.E., Gay N.J., Saraste M., Eberle A.N.;

"DNA sequence around the Escherichia coli unc of the sequence of a 17 kilobase segment containing the sequence of a 17 kilobase sequence of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP synthase delta chain (EC 3.6.3.14).
ATPH OR UNCH OR PAPE OR B3735 OR Z5233 OR ECS
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Hypothetical protein.
SEQUENCE 166 AA; 18390
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Hypothetical 18.4 kDa protein (ORF44).
Orgyla pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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Virology 229:381-399(1997).
-1- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV.
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Ahrens C.H., Russell R.R., Funk C.J.,
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                                                                                                                                                                                                                                                                    for the membrane proteins, ATP-synthase.";
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                                                                                                                                                                                                                                                                                                       operon: nucleotide sequence of the promoter and the gen membrane proteins, and the delta subunit of Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=6272190;
                                                                                                                                                                                                                                 9:3919-3926(1981).
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%; Pred. No. 30;
0; Mismatches
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   von Meyenburg K.;
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ane bound ATP synthase
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EMBL; AE000450; AAC76758.1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-0157.H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
Maxino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama M., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: Alpha(3), BETA(3), GAWAA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C. SIMILARITY: BELONGS TO THE ATPASE DELTA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEDLINE=97307253; PubMed=9164460;
MEDLINE=97307253; PubMed=9164460;
Wilkerns S., Duns S.D., Chandler J., Dahlquist F.W., Capaldi R.A.;
Wilkerns S., Duns S.D., Chandler J., Dahlquist F.W., Capaldi R.A.;
Wilkerns Structure of the N-terminal domain of the delta subunit of
the E. coli Arpeynthase.";
Nat. Struct. Biol. 4:198-201(1997).
-!- FUNCTION: THIS PROTEIN SEEMS TO BE PART OF THE STALK THAT LINKS
CF(0) TO CF(1). IT EITHER THANSMITS CONFORMATIONAL CHANGES FROM
CF(0) INTO CF(1) OR IS IMPLICATED IN PROTON CONDUCTION.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=93135143; PubMed=7686882;
Burlone V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
Burland V.D., Plunkett G. III, bakilobases of the Escherichia coli
Burlona sequence and analysis of 136 kilobases of the Escherichia coli
genome: organizational symmetry around the origin of replication.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                          MEDLINE-82068433; PubMed-6458296; Mabuchi K., Kanazawa H., Kayano T., Futai M.; Machochi K., Kanazawa H., Kayano T., Futai M.; Mucleotide sequence of the gene coding for the delta subunit of proton translocating ATPase of Escherichia coli."; Biochem. Biophys. Res. Commun. 102:172-179(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BOLD'STRY / EDL933 / ATCC 700927;
MEDLINE=1074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Rose D.J., Maybew G.F., Evans P.S., Gregor J., Kirkparrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grock E.J., Davis N.W., Lim A., Dimalanta E.T., Potemousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                        . Gen. Genet. 184:33-39(1981).
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V00266; CAA23524.1;
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L10328; AAA62087.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                              Genomics 16:551-561(1993)
Escherichia coli.";
                                                                        FROM N.A.
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-i- SIMILARITY: CONTAINS! I RGS DOWAIN.

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                                                                        PIR; A01031; PWECD.
PDB; 1ABV; 07-UTL-97.
ECGGENE; EGIOUS; atpr.
FROND: PRONO'11; ATPSYNT_OSCP.
PRINTS; PRO123; OSCP; 1.
PRINTS; PRO125; ATPASEDENTA.
TIGRAMS; PRO135; ATPASEDENTA.
PROSITE; PRO0389; ATPASE DELTA; 1.
Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Dorsal root ganglion;
MEDLINE=99348269; Pubmed=10419452;
Jordan J.D., Carey K.D., Stork P.J.S., Iyengar R.;
"Modulation of Rap activity by direct interaction of Galphao with Rapl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTPase-activating protein.";
J. Biol. Chem. 274:21507-21510 (1999).

-I- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
THEIR INACTIVE GDP-BOUND FORM.
-I- SUBCELLULAR LOCATION: Membrane-bound (Potential).
-I- PTM: FATTY ACYLATED. HEAVILY PALMITOYLATED IN THE CYSTEINE STRING
MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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Signal transduction inhibitor; Membrane; Lipoprotein; Palmitate.
DOMAIN 28 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 177;
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GAFD9552A79C81A5 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Regulator of G-protein signaling 17 (RGS17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.0%; Score 7; DB 1;
100.0%; Pred. No. 32;
tive 0; Mismatches
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Pfam; PF00615; RGS; 1.
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ProDom; PD001580; Reg of prG; 1.
SMART; SM00315; RGS; 1.
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                     AE005605; AAG58938.1;
AP002566; BAB38100.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                             Complete proteome.
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RGSH_CHICK
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).

-i- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING
-i- FUNCTION: OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING
                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Golackenbush Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peng B., Kochiwa H., Kuehl P., Kuehl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C3/D4/V0, PubMed=11217851;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Isnii
Kawai J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda
Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka
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SEQUENCE FROM N.A.

TISSUE=Olfactory bulb;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regulator of G-protein signaling 17 (RGS17) (Regulator of Gz-selective protein signaling 2). RGS17 OR RGS22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9QZB0;
16-OCT-2001
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EMBL; AF191555; AAF05758.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
                                                                                                                                                                                                                                                                                                                        THEIR INACTIVE GDP-BOUND FORM.
SUBCELLULAR LOCATION: Membrane-bound (Potential).
PTM: FATTY ACYLATED. HEAVILY PALMITOYLATED IN THE
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(Rel. 40, Last annotation updat
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L00.0%; Pred. No.
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EMBL/GenBank/DDBJ databases
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HSSP; P49795; 1CMZ.
MGD; MGI:1927469; Rgs17.
InterPro; IPR000342; Reg1_Gprotein.
Pfam; PF00615; RGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSDLINE=96172747; PubMed=8589412;
ROEST H.P., Mulders I.H.M., Wijffelman C.A.,
"Isolation of ropB, a gene encoding a 22-kDa
outer membrane protein.";
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the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                 InterPro; IPR000498; OmpA_tmem.
Pfam; PF01389; OmpA_membrane; 1.
                                                                                                                                                                                                                                                                                                                                      EMBL; X80767; CAA56751.1; -
                                                                                                                                                                                                                                                                                                                                                                                     or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Outer membrane.-!- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
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115
                                          209 GSVRGRV 215
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GSVRGRV 121
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                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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22 KDA OUTER MEMBRANE PROTEIN
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Rhizobium leguminosarum
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RESULT 21

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[1]
SEQUENCE FROM N.A.
MEDLINE=9024564; PubMed=2336399;
Jalajakumari M.B., Manning P.A.;
"Nucleotide sequence of the gene, ompW, encoding a 22kDa immunogenic outer membrane protein of Vibrio cholerae.";
Nucleic Acids Res. 18:2180-2180(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR; VCA0867; -. Signal; Outer memb
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                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00272; END; 2.
PROSITE; PS00270; ENDOTHELIN; 2.
Cleavage on pair of basic residues; Vasoconstrictor; Multigene family;
                                                                                                                                                      SEQUENCE FROM N.A.
MEDIJNE=95094302; PubMed=8001160;
Baynash A.G., Hosoda K., Giaid A., Richardson J.A., Emoto N.,
Hammer R.E., Yanagisawa M.;
"Interaction of endothelin-3 with endothelin-B receptor is essential
for development of epidermal melanocytes and enteric neurons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outer membrane protein W precursor.
OMPW OR VCA0867.
Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                             Cell 79:1277-1285(1994).
-!- FUNCTION: ENDOTHELINS ARE ENDOTHELIUM-DERIVED VASOCONSTRICTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE ENDOTHELIN/SARAFOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8911260872D6A713 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENDOTHELIN-3.
ENDOTHELIN LIKE.
BY SIMILARITY.
BY SIMILARITY.
                                  01-FEB-1996 (Rel. 33, Created)
10-FEB-1996 (Rel. 31, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Endothelin-3 precursor (ET-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last amoutation update)
16-OCT-2001 (Rel. 40, Last annotation update)
             214 AA
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Mismatches
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MGD, MGI.95285, Edn.
InterPro, 1PR001928; Endothelin.
InterPro, 1PR001928; Endothelin.
Pfam, PF00325, endothelin, 1.
PRINTS, PR00365, ENDOTHELIN, 1.
ProDom; PD005286; Endothelin; 1.
             PRT;
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
             STANDARD;
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117
173
111
107
                                                                                              Mus musculus (Mouse).
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Best Local Similarity
                                                                                                                              NCBI_TaxID=10090;
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OMPW_VIBCH
             MOUSE
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              ET3 MOU
P48299;
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  ET3 MOUSE
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-El Tor N16961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Vamayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
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                                                                                                                                                                                                                                                                                                            DNA sequence of both chromosomes of the cholera pathogen Vibrio
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100.0%; Pred. No. 38;
cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF376BB11EF2797B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OUTER MEMBRANE PROTEIN W.
                                                                                                                                                                                                                                                                                                                                                            Nature 406:477-483(2000).
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: TO E.COLI OMPW AND P.OLEOVORANS ALKL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISSING (IN REF. 1).

SS -> LA (IN REF. 1).

Q -> H (IN REF. 1).

A -> N (IN REF. 1).

F -> N (IN REF. 1).

G -> S (IN REF. 1).

AG -> NA (IN REF. 1).

AG -> Y (IN REF. 1).

AC -> Y (IN REF. 1).

AC -> Y (IN REF. 1).
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P39631;
01-FBE-1995 (Rel. 31, Created)
01-FBE-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Spore coat polysaccharide biosynthesis protein spsA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer membrane; Antigen; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE004414; AAF96765.1; -. PIR; S09509; S09509.
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Query Match

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7; Conserve
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210
217 AA;
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Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ghiseppi G., Guy B.J., Haga K., Haisch J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lepidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Takagi T., Takahashi H., Takemaru K.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Sorokin A., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Viari A., Vanamoto H., Yamane K., Yata K.,
Yata K.,
Yata K., Yata K.,
The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDDE F., USE Kunst F., USE P. P.
EMBL; X73124; CAA51619.1; -.
EMBL; Z99123; CAB15817.1; -.
PDB; 1QGQ; 21-APR-00.
PDB; 1QGQ; 04-MAY-00.
PDB; 1QGS; 04-MAY-00.
SubtiList; BG10609; 8psA.
InterPro; 1PR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Transferase; Glycosyltransferase; 3D-structure; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charnock S.J., Davies G.J.;

"Structure of the nucleotide-diphospho-sugar transferase, Sg. Bacillus subtilis, in native and nucleotide-complexed forms. Biochemistry 38:6380-6385(1999).

-i- FUNCTION: GLYCOSYLTRANSFERASE IMPLICATED IN THE SYNTHESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Boursier L., Brans A., Braun M., Brighell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Choi S.K., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Presecan E., Santana M., Schneider E., Schweizer J., Vertes A., Rapoport G., Danchin A.; "Bacillus subtilis genome project: cloning and sequencing of the kb region from 325 degrees to 333 degrees."; Mol. Microbiol. 10:371-384(1993).
                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glaser P., Kunst F.,
                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98044033;
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                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Spore coat
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete genome sequence
ilis.";
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TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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                                                                                                                                                                                                                                                                     Usage
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DE 4-4(1)
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30-MAY-2000 (Rel. 39, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L. Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Hube Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                 NP_BIND 88
                                                                                                                                                                                                                                                                                                         Pfam; PF00288; GHMP_kinases; 1.
TIGRFAMs; TIGR00154; ispE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents to the content is not removed.
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-!- FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POSITION 2 HYDROXY GROUP OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aeolicus
                                                                                                                                                                                                                                                                              Transferase; Kinase; Isoprene biosynthesis; ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000713; AAC07027.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Aquificae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001745; GHMPknse
InterPro; IPR004424; IspE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISPE OR AQ 915
                                                  586
  152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
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                                                  VETEISG
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                                                                                                   Similarity 7; Conser
                                                                                                                                                                                                 88
268 AA;
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256 AA;
                                                                                                     Conservative
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                                                  592
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                                                                                                                                                                                                      98 F
29788 MW;
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                           ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                    ATP
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                                                                                                                                                                                                      C905F9B98BE0B45D CRC64;
                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                   DB 1;
                                                                                                0;
                                                                                                                                                Length 268
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l kinase).
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                                                                                                   Gaps
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MEDLINE=97061201; PubMed=8905231;
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SEQUENCE 295 AA
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P14609;
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ID FEBB EACH
TO 11-APR
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6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: INVOLVED IN POTASSIUM TELLURITE RESISTANCE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=55350630, PubMed=7542800;
Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Morrick J.M.,
McKenney R., Bult C.J., Tomb J.-F., Dougherty B.A., Morrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kalley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geognagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable nicotinate-nucleotide pyrophosphorylase (carboxylating)
(EC 2.4.2.19) (Quinolinate phosphoribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR000051; SAM bind.
InterPro; IPR004537; TehB.
InterPro; IPR004537; TehB.
InterPams; IIGR00477; tehB: 1.
Antibiotic resistance; Tellurium resistance; Complete proteome.
SEQUENCE 286 AA; 33019 MW; 69D7647E97CC74FA CRC64;
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                                                                                                                                                                                                                                                                            Haemophilus influenzae.
Bacteria, Proteobacteria, gamma subdivision, Pasteurellaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 1; Length 286;
Pred. No. 48;
0; Mismatches 0; Indels
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                           01-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Tellurite résistance protein tehB homolog. TEHB OR HI1275.
                                                             286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 AA
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100.0%; Pre
                                                                                                                           (Rel. 32, Created)
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                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                           01-NOV-1995
                                                       TEHB HAEIN
P45134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NADC_SYNY3
P74301;
                             TEHB HAEIN
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NADC_SYNY3
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RESULT 25
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Kaneko I., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Okumura J., Matcuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S., Yamada M., Tabata S., Suguence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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"Nuclocitide sequence and regulation of the Escherichia coli gene for
"Retrienterobactin transport protein FepB.";
J. Bacteriol. 171:5443-5451(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                    diphosphate.
-!- PATHWAY: NAD biosynthesis; aspartate to NaMN; third (last) step.
-!- SIMILARITY: BELONGS TO THE NADC/MODD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyridine nucleotide biosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ferrienterobactin-binding periplasmic protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 AA; 31973 MW; DBCF6F88362E0735 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 1.0%; Score 7; DB 1;
Local Similarity 100.0%; Pred. No. 49;
nes 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D90914; BAA18395.1; -. HSSP; P30012; 1QAP.
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Interpro; IPR002638; QRPTase
Pfam; PF01729; QRPTase; 1.
Pfam; PF02749; QRPTase_N; 1.
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TIGREAMs; TIGR00078; nadC; 1
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Best Local S
Matches '7
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P57856;
16-OCT-2001
16-OCT-2001
15-JUN-2002
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Stephens D.L. Choe M.D., Earhart C.F.;

"Bscherichia coli periplasmic protein FepB binds ferrienterobactin.";

"Bscherichia coli periplasmic protein FepB binds ferrienterobactin.";

"Brendey 141.1647-1654(1995)

-i- FUNCTION: BINDS FERRIENTEROBACTIN; PART OF THE BINDING-PROTEIN-

DEPENDENT TRANSPORT SYSTEM FOR UPTAKE OF FERRIENTEROBACTIN.

-i- SUBCELULAR LOCATION: PERIPLASMIC.

-i- INDUCTION: CONTROLLED IN PART BY THE AMOUNT OF AVAILABLE IRON.

-i- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
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between
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MEDLINE=90230305; PubMed=2139473;

Brickman T.J., Ozenberger B.A., McIntosh M.A.;

"Regulation of divergent transcription from the second control of the second control of
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               Bacteria; Proteobacteria;
Pasteurella.
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Pfam; PF01497; Peripla_BP_2; 1.
Transport; Iron transport; Signa
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EMBL; U82598; AAB40791.1; --
EMBL; X53274; CAA37370.1; --
PIR; JV0045; JV0045
EcoGene; EG10294; fepB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chung E., Allen E., Araujo R., Aparicio A., Davis K., Dunc Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lev Namath A., Oefner P., Roberts D., Schramm S., Davis R.W., Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                  Anthranilate phosphoribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M29730; AAA83853.1; -.
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nce 277:1453-1474(1997).
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(Rel. 42, Last annotation update)
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ilarity 100.0%;
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Signal; Periplasmic;
POTENTIAL.

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Pred. No. 53;
0; Mismatches
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                                     subdivision;
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53;
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                                     Pasteurellaceae;
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RESULT 29
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Matches
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May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-i- CATALYTIC ACTIVITY: Anthranilate + phosphoribosylpyrophosphate =
-i- CATALYTIC ACTIVITY: Anthranilate + diphosphate.
-i- PANTWAY: Tryptophan biosynthesis; second step.
-i- PANTWAY: Tryptophan biosynthesis; second step.
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SEQUENCE FRO
STRAIN=Pm70;
                                                                                          Rleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkne Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merri McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J. Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandc Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE006093; AAK02665.1; -. InterPro; IPRO00312; Glycos transf 3. Pfam; PF00591; Glycos transf 3; 1. Pfam; PF02885; Glycos trans 3N; 1. ProDom; PD001864; Glycos transf 3; 1. ProDom; PD001864; Glycos transf 3; 1. ProDom; PD005916; Thymid phosphls; 1.
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                                                                                   Fine L.D., Fritchman J.L.,
Gnehm C.L., McDonald L.A.,
Venter J.C.;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995
15-JUN-2002
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Complete proteome.
SEQUENCE 333 AA; 35880
                          Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
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PATHWAY: Arginine
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32, Last sequence update)
41, Last annotation update)
""" ransferase, catabolic (EC
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V., Fraser C.M., Smith H.O
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                                                                     assembly
arginine
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RAY MEDLINE=21848401; PubMed=11859360;

RAY WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RAY Squores U., Peat N., Hayles J., Basham D., Bowman S.,

RAY Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RAY Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RAY Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RAY Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RAY Holroyd S., Mungall K., Murphy L., Nibheth D., Odell C.,

RAY Noney P., Moule S., Ranson D., Quail M.A., Rabbinowitsch E.,

RAY Ritherford K., Rutter S., Sanders D., Seeger K., Sharp S.,

RAYOR K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RAYOR K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RAYOR K., Langer I., Beck M., Schaefer M., Mueller-Auer S.,

RAY Gobel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RAY BOTZUM K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RAY Gable C., Kords W., Wedler H., Wambutt R., Purnelle B.,

RAY Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RAY Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Baga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
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                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                  1.0%; Score 7; DB 1; Length 334;
100.0%; Pred. No. 55;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                        e; Arginine metabolism; Complete proteome.
334 AA; 37647 MW; B44B9ED2CIBB57F5 CRC64;
             -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetae;
Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UND-2002 (Rel. 41, Last annotation update)
15-UND-2002 (Rel. 41, Last annotation update)
SPAC2267.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 AA
                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGRO0658; orni carb tr; 1.
PROSITE; PS00097; CARBAMOVLTRANSFERASE; 1.
SUBUNIT: HOMOTRIMER (BY SIMILARITY).
                                                                                                                                                                                                                  InterPro; IPR002029; Asp/Orn Cotranf.
InterPro; IPR002292; Orn carbtransf.
Pfam; PF00185; OrCace; 1.
Pfam; PF001729; OrCace, N. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                       EMBL; U32741; AAC22253.1; -. HSSP; P08308; 10RT.
                                                                                                                                                                                                                                                                            PRINTS; PR00100; AOTCASE.
                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             637 YQVTPEL 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 YQVTPEL 260
                                                                                                                                                                                                      TIGR; HI0596; -
                                                                                                                                                                                                                                                                                                                          Transferase;
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Q09801;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Forsburg S.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spierings G., Ockhuijsen C., Hofstra H., Tommassen J.;
"Characterization of the Citrobacter freundii phoE gene and
development of C. freundii-specific oligonucleotides.";
FEMS Microbiol. Lett. 78:199-204 (1992)
-!- FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN CELLS ARE
GROWN UNDER PHOSPHATE LIMITATION. ITS ROTEIN PORE IS
PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC PHOSPHATE,
PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIVELY CHARGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 344 AA; 37290 MW; 571D391D0F88F27D CRC64;
                       Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Sous
Shpakovski G.V., Ussery D., Barrell B.G., Nurse, P.,
"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.0%; Score 7; DB 1;
100.0%; Pred. No. 56;
tive 0; Mismatches
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15-DEC-1998 (Rel. 37, Last annotation update)
Outer membrane pore protein E precursor.
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InterPro; IPR001329; OMP.2.
InterPro; IPR001702; PorIn gram-ve.
Pfam; PP00267; Gram-ve_porIns; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93146376; PubMed=1337052;
                                                                                                                                                                                    -!- SIMILARITY: TO YEAST FIP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z54328; CAA91134.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Citrobacter freundii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 7; Conserv
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Query Match
Best Local Similarity
Thes 7; Conserv
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MURB_TREPA
                                                                               Query Match
Best Local S
Matches 7
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15-DEC-1998
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spirochete.";
Science 281:375-388(1998).
-:- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
-:- CATALYTIC ACTIVITY: UDP-N-acetylmuramate + NADP(+) =
acetyl-3-O-(1-carboxyvinyl)-D-glucosamine + NADPH.
-:- COPACTOR: FAD (BY SIMILARITY).
-:- PATHWAY: Peptidoglycan biosynthesis.
-:- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-:- SIMILARITY: BELONGS TO THE MURB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeodd M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S. Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
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MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Last annotation update) UDP-N-acetylenolpyruvoylglucosamine reductase
                                                                                                                                                                             InterPro; IPR003170; MurB.
InterPro; IPR003170; MurB.
InterPro; IPR001575; Oxid_FAD_bind.
Iffam; PF02565; FAD_binding_4; 1.
Pfam; PF02873; MurB_C; 1.
Pfam; PF02873; MurB_C; 1.
Peptidoglycan synthesis; Cell wall; Cell division; Oxidoreductase;
NADP; Plavoprotein; FAD; Complete proteome.
NADP; Plavoprotein; FAD; Complete proteome.
SEQUENCE 354 AA; 38595 MW; 809E56E606F5BFF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Su or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MURB
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001193; AAC65086.1; -. TIGR; TP0090; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MURB OR TP0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acetylmuramate dehydrogenase).
461 LSLIGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in lifted and this statement is not removed. Usage by and for contents are not removed.
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                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spirochaetales; Spirochaetaceae; Treponema
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(Rel. 37, Last sequence update)
(Rel. 41, Last annotation updat
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100.0%; Pred. No.
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100.0%; Pred. No
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                                                                               Mismatches
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                                                                                                         DB 1;
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                                                                                                                                   Length 354;
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                                                                               Indels
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RESULT 34
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Best Local :
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                                                                               IPAC SHIDY
Q03946;
01-FEB-1994
01-FEB-1994
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P23164;
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CONFLICT
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Shigella dysenteriae Plasmid Invasion.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M57545; AAA42678.1; -.
EMBL; U18466; AAA65382.1; -.
PIR; F43680; F43680.
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MEDLINE=90219205; PubMed=2325203;
Gonzalez A., Calvo V., Almazan F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          African swine fever virus (strain BA71V) (ASFV)
Viruses; dsDNA viruses, no RNA stage; Asfarviri
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01-NOV-1995 (Rel. 32, Last ann
                                               42 kDa
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Rodriguez J.F., Vinuela E.;
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                                 IPAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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                                                                 30-MAY-2000
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InterPro; IPR002595; ASFV_360.
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                                                             28, Created)28, Last sequence update)39, Last annotation updat
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4841A8165647BFE3 CRC64;
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Ittmann M.;
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-!- FUNCTION: ASSOCIATED WITH THE ENTRY OF THE BACTERIA INTO COLONIC EPITHELIAL CELLS.
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BUDNELSE89957927; PubMed=31057506;
Venkatesan M.M., Buyses J.M., Kopecko D.J.;
"Characterization of invasion plasmid antigen genes (ipaBCD) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shigella flexneri.
Plasmid 210 kb invasion pWR100, and Plasmid 230 kb pMYSH6000.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                         Yao R., Palchaudhuri S.;
"Nucleotide sequence of the ipaBCD structural genes of Shigella
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STRAIN-SEACOCYPE 2A, PLASMID=230 kb pMYSH6000;
MEDLINE=90014179; PubWed=2552264;
Sasakawa C., Adler B., Tobe T., Okada N., Nagai S., Komatsu K.,
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100.0%; Pred. No. 62;
cive 0; Mismatches 0; Indels
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"Nucleotide sequence of the invasion plasmid antigen B
(ipaB and ipaC) of Shigella flexneri.";
Microb. Pathog. 4:345-357(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 KDA MEMBRANE ANTIGEN.
A22E1D6399EC90BF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen; Plasmid; Virulence; Membrane; Signal. SIGNAL 1 19 BY SIMILARITY.
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01-NOV-1990 (Rel. 16, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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42 kDa membrane antigen precursor.
                                                                                                                      MEDLINE=92114800; PubMed=1766387;
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MEDLINE=89200844; PubMed=3071655;
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                     Shigella.
NCBI_TaxID=622;
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"Isolation of the human gene that complements a temperature-sensitive
cell cycle mutation in BHK cells.";
Mol. Cell. Biol. 7:3386-3393(1987).
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                                                                                                                        PARTIAL SEQUENCE OF 20-64 AND 318-335.
MEDLINE-89307550; PubMed-2663721;
Sankaran K., Ramachandran V., Subrahmanyam Y.V.B.K., Rajarathnam S.,
                                                                                                                                                                                                                                                                                                         Infect. Immun. 57:2364-2371(1989).
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"Functional organization and nucleotide sequence of virulence Region-2 on the large virulence plasmid in Shigella flexneri 2a."; Mol. Microbiol. 3:1191-1201(1989).
                                                                                                                                                                                                                                                                                                                                                                        EPITHELIAL CELLS.
-!- MISCELLANEOUS: SYNTHESIS OF THIS IMMUNOGEN IS REPRESSED AT 30 DEGREES CELSIUS AND RESTORED AT 37 DEGREES CELSIUS.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                    Elango S., Roy R.K.; "Congo red-mediated regulation of levels of Shigella flexneri 2a
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100.0%; Pred. No. 62;
iive 0; Mismatches 0; Indels
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01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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EMBL; M34849; AAA98425.1; ALT_INIT.
EMBL; X15319; CAA33382.1; -.
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Homo sapiens (Human).
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MEDLINE=92295566; PubMed=1318606;
Telford E.A.R., Watson M.S., McBride
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
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/irology 189:304-316(1992).
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Kinkou M., Fukushi H., Matsumura T., Kim S.K., O'Callagh Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE=92263758; PubMed=1316673; Colle C.F. III, Flowers C.C., O'Callaghan D.J.; Colle C.F. III, Flowers C.C., O'Callaghan D.J.; Open reading frames encoding a protein kinase, hom glycoprotein gX of pseudorables virus, and a novel within the unique short segment of equine herpesvir Virology 188:545-557(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                              Essenberg R.C., Candler C., Nida S.K.;

"Brucella abortus strain 2308 putative glucose and galactose
transporter gene: cloning and characterization.";

Microbiology 143:1549-1555(1997).

-i- FUNCTION: INTAKE OF GLUCOSE AND GALACTOSE (POTENTIAL).

-i- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                       Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group,
Brucellaceae, Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Nichols;
MEDLINE=9833270; PubMed=9665876;
Fraser C.W., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.0%; Score 7; DB 1; Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                716D3AAB9E197E5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacieria, Spirochaetales, Spirochaetaceae, Treponema
NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                          Sugar transport; Transmembrane; Inner membrane. TRANSMEM 21 41 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein TP0118.
       15-JUL-1998 (Rel. 36, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Glucose/galactose transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 AA
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                                                                                                                     MEDLINE=97311994; PubMed=9168605;
Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  43859 MW;
                                                                                                                                                                                                                                                                                                      EMBL; U43785; AAB58958.1; -. TIGRFAMS; TIGR01272; glup; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                              259
330
351
383
408
                                                                                                                                                                                                                                                                                                                                                                                                                            363
388
412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                   SEQUENCE FROM N.A.
                                                Brucella abortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 KALAFDA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 KALAFDA 310
                                                                                NCBI_TaxID=235;
                                                                                                                                                                                            (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y118 TREPA
083155;
16-OCT-2001 (
16-OCT-2001 (
                                                                                                             STRAIN=2308;
                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- CATALYTIC ACTIVITY: ATP + {tetrahydrofoly1-[Glu]}(N) + L-glutamate
= ADP + phosphate + {tetrahydrofoly1-[Glu]}(N+1).
-!- PATHWAY: BACTERIA REQUIRE FOLATE FOR THE BIOSYNTHESIS OF GLYCINE,
METHIONINE, FORMYL-MET-TRNA, THYMIDYLATES, PURINES, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole-genome random sequencing and assembly of Haemophilus influenzae
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalard H., Richardeon D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujil C., Garland S. Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95350630; PubMed=7542800; Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Rerlavage A.R., Bult C.J., Tromb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE FOLYLPOLYGLUTAMATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 269:496-512(1995).
-!- FUNCTION: CONVERSION OF FOLATES TO POLYGLUTAMATE DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                   'Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein, Coiled coil, Complete proteome, DOMAIN 126 182 COILED COIL (POTENTIAL), DOMAIN 328 397 COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.0%; Score 7;
100.0%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001197; AAC65114.1; -.
TIGR; TP0118; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 AA; 46702 MW;
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1 / KW20 / ATCC 51907;
                                                                                                                                                                                                                                                        Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100...
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 AALGKRV 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOLC OR HI1261
                                                                                                                                                 Venter J.C.;
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RESULT 42
UVSH_EMENI STANDARD; PRT; 443 AA.
ID UVSH_EMENI STANDARD; PRT; 443 AA.
AC Q02398; Q00178;
DT 15-JUN-2002 (Rel. 41, Cast sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sannotation update)
DE Postreplication repair protein uvsH/nuvA.
GN UVSH OR NUVA.
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Best Local S
Matches
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HSSP; P15925;
TIGR; HI1261;
                                                                                       This SWI
between
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Mol.
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InterPro; IPR000713; Mur_ligase.
Pfam; PF01225; Mur_ligase; 1
PROSITE; PS01011; FOLYLPOLYGLU SYNT_1; 1.
PROSITE; PS01012; FOLYLPOLYGLU SYNT_2; 1.
PROSITE; PS01012; FOLYLPOLYGLU SYNT_2; 1.
Ligase; One-carbon metabolism; ATP-binding; Comp.
NP_BIND 55 61 ATP (BY SIMILARITY)
            use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See l
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        Iwanejko L.A., Cotton C.M., Jones G.W., Tomsett A.B., Strike P., "nuvA, an Aspergillus nidulans gene involved in DNA repair and recombination, is a homologue of Saccharomyces cerevisiae RAD18 ..."
                                                                                                                                                                                                                                                                                                                        SEQUENCE OF
STRAIN=L20;
                                                                                                                                                                                                                                                                                                                                                                                        "The Aspergillus uvsH gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the
                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                             Microbiology 142:505-515(1996).
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95379762; PubMed=7651340; Yoon J.H., Lee B.J., Kang H.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=FGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        MEDLINE=97022065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 AATVLAA
                                                                                                                                  SUBCELLULAR LOCATION: Nuclear (By similarity). SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                            FUNCTION: Involved in postreplication repair of Postreplication repair functions in gap-filling strand on replication of damaged DNA. Has ssDNA
                                                                                                                                                                                                                                                                                                                                                                                   Neurospora UVS-2
                                                    SWISS-PROT entry is copyright. It is produced through a collabeen the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conserv
                                                                                                                                                                  similarity)
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                                                                                                                                                                                                                                                                                                                                      OF 1-356 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   437 AA;
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profit institutions as long as i
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                                                                                                                                                                                                                                                                                                                                                                   248:174-181(1995)
                                                                                                                                                                                                                                                                                                      PubMed=8868425;
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                         Noved. Usage by and for (See http://www.isb-sib.
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g of a daughter
h binding activity
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                                                                                       collaboration -
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RESULT
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Best Local S
Matches 7
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InterPro; IPR003034; SAP.
InterPro; IPR001841; Znf_ring.
Pfam; PP00097; Zf-C3HC4; 1.
Pfam; PP02037; SAP; 1.
SMART; SM00184; RING; 1.
SMART; SM00513; SAP; 1.
TIGRPAMS; TIGR00599; rad18; 1.
PROSITE; PS00518; ZF_RING 1; 1.
PROSITE; PS00518; ZF_RING 2; 1.
ZNO-finger; DNA-binding; DNA damage; DNA DING-TYPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - AQUAE
- SR54 AQUAE
- O67615;
- 30-MAY-2000
- 30-MAY-2000
                                                                                                                                                                                                                                                                                                                               STRAIN=VF5;
MEDLINE=98196666; PubMed=9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lend Deckert G., Warren P.V., Gaasterland T., Young W.G., Lend Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M. Graham D.E., Overbeek R., Snead M.A., Swanson R.V.;
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal recognition FFH OR AQ_1720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
HSSP;
                                                               This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
Signal recognition particle protein (Fifty-
                        EMBL; AE000753;
HSSP; O07347; 11
                                                                                                                                                                                                                          <del>-</del>
                                                                                                                                                                                                                                                                                             Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                         aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Aquificae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aquifex aeolicus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 LIANARK 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424 LIANARK 430
                                                                                                                                                                           FUNCTION: NECESSARY FOR EFFICIENT EXPORT OF EXTRA PROTEINS. BINDS TO THE SIGNAL SEQUENCE WHEN IT EM RIBOSOMES (BY SIMILARITY).

SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF MOLECULE AND PROTEIN FFH (BY SIMILARITY).

MOLECULE AND PROTEIN HAS A TWO DOMAIN STRUCTURE: T BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BI SEQUENCE.

SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S79392; AAB35098.1;
Z49875; CAA90033.1;
P15919; 1RMD.
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Conservative
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                                       AAC07579.1; -.
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270
210
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                                                                                                                                                                               TO THE SRP FAMILY OF GTP-BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7;
Pred. No.
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(Fifty-four
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                                                                               http://www.isb-sib.ch/announce/
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IT EMERGES FROM TE
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                                                                                                                                                                                                           BINDS
                                                                                                                                                                                                           THE G-DOMAIN
BINDS THE SIGNAL
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ay M., Huber
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                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Elongation factor 1-alpha (EF-1-alpha) (50 kDa actin-binding protein)
                                                                                                                                                                                                                               Gaps
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SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elongation factor 1a.";
Nature 347:494-496(1990).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DUBING PROTEIN BIOSYNTHESIS. IT IS ALSO AN ABUNDANT ACTIN FILAMENT BUNDLING
                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang F., Demma M., Warren V., Dharmawardhane S., Condeelis J.; "Identification of an actin-binding protein from Dictyostelium
                                                                                                                                                                                                       1.0%; Score 7; DB 1; Length 454;
100.0%; Pred. No. 71;
ive 0; Mismatches 0; Indels
                                                                                                                         289 G-DOMAIN.
454 M-DONAIN.
109 GTP (BY SIMILARITY).
186 GTP (BY SIMILARITY).
245 GTP (BY SIMILARITY).
50911 MW, 9F13FA8C883A0558 CRC64;
        InterPro; IPR004780; SRP eub.
Pfam; PF00448; SRP54; 1.
Pfam; PF02978; SRP54; 1.
Pfam; PF02978; SRP54; 1.
ProDom; PD000819; SRP54; 1.
SMART; SM00382; AAA; 1.
TIGRFAM9; TIGR00599; 38501801; 1.
PROSITE; PR0300; SRP54; 1.
Signal recognition particle; GTP-binding; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium
NCBI_TaxID=44669;
                                                                                                                                                                                                                                                                                                                                     456 AA
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                                                                                                                                                                                                                                                                                                                                     PRT;
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MEDLINE=91015340; PubMed=2215665;
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DictyDb; DD01027; efaA.
InterPro; IPR004539; EF1 alpha.
InterPro; IPR004160; EFTU_Cterm.
InterPro; IPR004161; EFTU_D2.
InterPro; IPR004161; EFTU_D2.
  InterPro; IPR004125; SRP54_SPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X55972; CAA39442.1; -. EMBL; X55973; CAA39443.1; -. PIR; S11665; S11665.
                                                                                                                                                                                                                   Local Similarity 100.
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                       454
109
188
245
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102 1
184 1
242 2
454 AA;
                                                                                                                  Complete proteome.
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P18624;
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NP BIND
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Matches
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NCBI_TaxID=2787;
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF0114; GTP_EFTU D3; 1.
PRO1144; GTP_EFTU D2; 1.
PRO1144; GTP_EFTU D2; 1.
PRON125; PR00131; ELONGATNFCT.
TIGRPAMS; TIGR00483; EF-1 alpha; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
PROSITE; PS00301; PFACTOR_GTP; 1.
PROSITE; PS00301; PFACTOR_GTP; 1.
NP_BIND 17 24 GTP (BY SIMILARITY).
NP_BIND 156 159 GTP (BY SIMILARITY).
SEQUENCE 456 AA; 50066 MW; BCFE9ELB70C3D8A8 CRC64;
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Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
BINDS TWO MOLES OF GTP, OND AT AN EXCHANGEABLE SITE ON THE BETA
CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
-!- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
-!- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
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InterPro: IPR002453; Beta tubulin.
InterPro: IPR000217; Tubulin.
InterPro: IPR00017; Tubulin.
InterPro: IPR00017; Tubulin.
IPR00011; tubulin, 1.
IPR01161; TUBULIN.
IPROSITE; PS00226; TUBULIN.
IPROSITE; PS00226; TUBULIN.
IPROSITE; PS00226; TUBULIN.
IPROSITE; PS00226; TUBULIN.
IPPOSITE; PS00226; TUBULIN.
IPPOS
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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tes 7; Conserv
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Patent No. 5882851

GENERAL INFORMATION:

APPLICANT: Koch, Birgit M.
APPLICANT: Halkier, Barbara Ann
APPLICANT: Halkier, Barbara Ann
APPLICANT: Moller, Birger L.

TITLE OF INVENTION: Cytochrome P-450 Monooxygenases
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5882851artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
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ZIP: 27709
ZIP: 27709
COMPUTER LEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/656,177A
FILING DATE: 08-AUG-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAMME: Meigls, J. Timothy
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: S-19783/A/PCT
TELECOMMUNICATION NUMBER: S-19783/A/PCT
TELECOMMUNICATION NUPORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEC 1D NO: 3:
SEQUENCE CHARACTERISTICS:
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US-08-602-999A-88
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                                                                                                             US-09-256-797-3
; Sequence 3, Application US/09256797
; Patent No. 6133417
; GENERAL INFORMATION:
; APPLICANT: Koch, Birgit M.
; APPLICANT: Koch, Birgit M.
; APPLICANT: Barbera Ann
APPLICANT: Moller, Barbara Ann
APPLICANT: Moller, Birger L.
; TITLE OF INVENTION: Cytochrome P-450 Monooxygenases
; UMMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6133417artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
      Length 17;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/256,797
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/656,177
FILING DATE: 08-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Majgs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 3-19783/A/PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 3:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LEMECHA! 17 Amino acids
  1.0%; Score 7; DB 2
100.0%; Pred. No. 7.1
ive 0; Mismatches
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100.0%; Pred. No. 7.1
cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / CECULGY: linear
// MOLECULE TYPE: protein
// HYPOTHETICAL: NO
// ANTI-SENSE: NO
// FRAGMENT TYPE: N-terminal
US-09-256-797-3
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MEDIUM TYPE: Floppy disk
Query Match
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Loca 7; Conservative
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US-08-817-811-97
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US-08-817-811-21
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             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 75 amino acids
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PRIOR APPLICATION DATA:
APPLICATION UNDER: WO 96/11944
PILING DATE: 25-APR-1996
PILING DATE: 15-APR-1196
NUMBE: 415-APR-110N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                       TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES TITLE OF INVENTION: COMPRISING SAME NUMBER OF SEQUENCES: 97
                                                                                                                                                                                                                                                                           APPLICANT: Relf, Wendy A.
APPLICANT: Good, Michael F.
APPLICANT: Saul, Allan J.
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nes 7; Conserv
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TOPOLOGY: li
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STATE: Texas
                                                                                                                                                               STREET:
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REFERENCE/DOCKET NUMBER: FBRC:005
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ZIP: 77210
                                                                                                     COUNTRY:
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                                                                                                                                                Houston
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                                                                                                                              Texas
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P.O. Box 4433
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P.O. Box 4433
                                                                                                           USA
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PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                White & Durkee
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100.0%; Pred. No. 26
ive 0; Mismatches
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RESULT 5
US-08-817-811-20
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Best Local Similarity 100.
""" Conservative
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             TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 96
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
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LENGTH: 76 amino acids
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APPLICATION NUMBER: WO 9:
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                            TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US
FILING DATE: 14-APR-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES TITLE OF INVENTION: COMPRISING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 ARGGLAL 413
                                                                                        NAME: Highlander, Steven REGISTRATION NUMBER: 37, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
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ZIP: 77210
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                                                           TELEPHONE:
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ENGTH:
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                                                                                                                            Highlander, Steven L
                                                                                                                                                                                                                                                                                                                                                                                             Texas
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P.O. Box 4433
78 amino acids
                                               512/474-7577
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Good, Michael F.
                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.30
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                                                             512/418-3000
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100.0%; F1
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                                                                                                           37,642
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ER: FBRC:005
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                                                                                               FBRC: 005
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5. 27;
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TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
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US-08-817-811-96
US-08-817-811-96
Sequence 96, Application US/08817811
Sequence No. 6174528
GENERAL INFORMATION:
APPLICANT: Cooper, Juan A.
APPLICANT: Relf, Wendy A.
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
TITLE OF INVENTION: COMPRISING SAME
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
                                                1.0%; Score 7; DB 4; Length 78;
100.0%; Pred. No. 27;
cive 0; Mismatches 0; Indels
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100.0%; Pred. No. 27;
tive 0; Mismatches
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INFORMATION FOR SEQ ID NO: 96: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 7; Conservative
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27 ARGGLAL 33
; STRANDEDNESS:
; TOPOLOGY: li
US-08-817-811-20
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TOPOLOGY:
US-08-817-811-96
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US-08-817-811-95
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APPLICANT: IWANAGA, SADAA
APPLICANT: MUTA, TATSUSHI
                                                            TELEFAX: (617) 248-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 512/474-7577 INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 96/11944
FILLING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
                           SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS;
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ODA, TOSHIO
TITLE OF INVENTION: NOVEL PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: FBRC:005
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407 ARGGLAL 413
                                                                                                                                                                                                           APPLICATION NUMBER: US/08/392,828C FILING DATE: 28-FEB-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 ARGGLAL 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.0%;
nes 7; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 14-AP
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOVEL POLYPEPTIDE AND DNA ENCODING
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                                                                                                                                         32,503
ER: FJN-033
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                                                                                                                                                                                                                                                                                Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
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문
                                                         ; LOCATION: 1.127
; OTHER INFORMATION:
US-09-330-945-39
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US-09-330-945-39
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Best Local Similarity 100.
Thes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 39, Patent No. 6
                             Query Match
                                                                                                                                                                                                     TELEPHONE: (617) 248-700
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/119,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: FJ
                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                      FEATURE:
                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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/ Match 1.0%; Score 7; DB 3;
Local Similarity 100.0%; Pred. No. 42;
nes 7; Conservative 0; Mismatches
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OTHER INFORMATION: /note= "XLN A SEQUENCE (FIGURE 4)"
                                                                                                                                                STRANDEDNESS: sin TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                   NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/330,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                           ENGTH:
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6077946
                                                                                                                                                                             amino acid
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STON
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SEKI, NORIAKI
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100.0%; Pr/
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                                                                        /note= "XLN A SEQUENCE (FIGURE 4)"
                                                                                                                                                                                                                                                                                                  27,829
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Pred. No.
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                           Length 127;
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 Indels
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Gaps
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APPLICANT: Boston, Rebecca S.
APPLICANT: Bass, Henry W.
APPLICANT: O'Brian Gregory R.
TITLE OF INVENTION: DA Encoding A Ribosome Inactivating TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genneth D. Sibley; Bell, Seltzer, Park and ADDRESSEE: Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 278;
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STREET: Post Office Drawer 34009
CITY: Charlotte
STRATE: No. 5552140th Carolina
COUNTRY: U.S.A.
ZIP: 28234
COMPUTER: Lababale FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/279,996
FILING DATE: 25-UUL-1994
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 07/941,651
FILING DATE: 08-5EP-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,665
REPERBNCE/DOCKET NUMBER: 31,665
REPERBNCE/DATION NUM
                                     .;
0
     100.0%; Pred. No. 83; ative 0; Mismatches
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Pred. No.
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US-08-746-797-2
; Sequence 2, Application US/08746797
; Patent No. 5759832
; GENERAL INFORMATION:
; APPLICANT: Gentry, Daniel
; APPLICANT: Lonsdale, John
; APPLICANT: Payne, David
; APPLICANT: Pearson, Stewart
                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08279996
Patent No. 5552140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.0%; Scc
illarity 100.0%; Pr
Conservative 0;
                                   7; Conservative
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Best Local Similarity
Matches 7; Conservi
Best Local Similarity
Matches 7; Conserv
                                                                                       558 KDKNAAA 564
                                                                                                                                               262 KDKNAAA 268
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US-08-279-996-2
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Sequence 2, Application US/07941651

Patent No. 5332808

Patent No. 5332808

APPLICANT: Boston, Rebecca S.
APPLICANT: Bass, Henry W.
TITLE OF INVENTION: DNA Encoding A Ribosome Inactivating TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCES: 6
CORRESPONDENCES: 6
CORRESPONDENCES: 6
CORRESPEE: Glabon
STREET: Post Office Drawer 34009
COUNTRY: U.S.A.
                                                                                                                                                          SESSUA.

STREAM

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PACENT NO. 5182262

PACENT NO. 5182262

APPLICANT: LETO, THOMAS

TITLE OF INVENTION: CALMODULIN BINDING PEPTIDE DERIVATIVES

OF NON-ERYTHROID ALPHA SPECTRIN

NUMBER OF SEQUENCES: 15

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/318,172

FILING DATE: 02-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 248;
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ZIP: 28234
COMPUTER 182824
COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,651
FILING DATE: 19920908
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SIDLEY, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-199
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECEX: 575102
TELEEX: 575102
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
'FWATTH: 278 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.0%; Score 7; DB 6
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches
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AMINO ACID
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        205 LNSDGSV 211
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                                           LNSDGSV
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Length 278;

DB 1;

Score 7;

1.0%;

Query Match

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; ANTI-SENSE: NO
; FRAGMENT TYPE: 1
; ORIGINAL SOURCE:
US-08-746-797-2
                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08927387 Patent No. 5783432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Gentry
                                                                                                                                                                                                                                                                                                                                     08-927-387-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 5759832 Yet Assigned FILING DATE: 23-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL FABH
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                               APPLICANT: Pearson, Stewart
TITLE OF INVENTION: NOVEL FabH
                                                                                                                                                                                                                                  APPLICANT: Payne, David
                                                                                                                                                                                                                                                                                                                                                                                                  178 SLNSDGS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                     204 SLNSDGS 210
                                                                                                             STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 709 Swedeland Road CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/746,797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
OPERATING SYSTEM:
                                                                19406-0939
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                                                                                U.S.A.
                                                                                                                                                                                                                                                   Lonsdale, John
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                                                                                                                                                                                                                                                                   Gentry, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
IBM Compatible YSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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100.0%; Pred. No.
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                                                                                                                                  Road
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o. 95;
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-927-387-2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,058
FILLING DATE: 25-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/746,797
FILLING DATE:
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
             ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/746,797
FILING DATE: 23-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pearson, Stewart
TITLE OF INVENTION: NOVEL FabH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 SLNSDGS 184
ELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                        CITY: King of Prussia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                            TRY: U.S.A.
19406-0939
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Payne, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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100.0%; Pr
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0; Mismatches
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             PS0573
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Sequence 3, 2020-3304-3
Sequence 3, 5920-37
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Sequence 3, Application US/09267384

Patent No. 613944

GENERAL INFORMATION:

APPLICANT: CRABB, Brendan S.

APPLICANT: STUDBERT, Michael J.

TITLE OF INTENTION: BOUINE HERPESVIRUS GLYCOPROTEINS

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500
Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.0%; Score 7; DB 2
100.0%; Pred. No. 1.2
ive 0; Mismatches
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 7; Conservative
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US-08-338-530A-3
                                                                              362 KQKALAF 368
                                                                                                                                   60 KOKALAF 66
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US-08-338-530A-3
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Sequence 52, Application US/08921887

Batent No. 603071

GENERAL INFORMATION:
APPLICANT: KHUDYAKOV, YURI E.
APPLICANT: FIELDS, HOWARD A.
TITLE OF INVENTION: MOSAIC PROTEIN AND RESTRICTION
TITLE OF INVENTION: ENDONUCLEASE ASSISTED LIGATION METHOD FOR MAKING THE SAME NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: JONES & ASKEW, LLP
STREET: 191 Peachtree Street, N.W., 37th Floor
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CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/921,887
FILING DATE:
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: WARREN, WILLIAM L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 36,714
TELEPHONE: 404-818-3790
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS: not relevant not relevant
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                                                                        INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
TYPE: amino acid
STRANDEDNESS: single
  610-270-4478
                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 7; Conservative
                      TELEFAX: 610-270-5090
TELEX:
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                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
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  TELEPHONE:
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CURRENT APPLICATION NUMBER: US/09/457,046B;
CURRENT FILING DATE: 1999-12-07;
NUMBER OF SEQ ID NOS: 74;
SOPTWARE: PatentIn Ver. 2.1;
SEQ ID NO 64;
LENGTH: 461;
TYPE: PRT;
ORGANISM: Arabidopsis thaliana
US-09-457-046B-64
                RESULT 21
US-08-468-812-8
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                                                                                                                            Query Match
Best Local Similarity lou.
"---hes 7; Conservative
Sequence 8, Application US/08468812
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 64, Application US/09457046B Patent No. 6287835
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40268/120/CSMB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/338,530
FILING DATE: 25-JAN-1995
APPLICATION NUMBER: WO PCT/AU93/00
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                      277
                                                                                                                   668 TFDAMAA 674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 TVLAALS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington STATE: D.C.
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                                                                                 TFDAMAA 283
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28-MAY-1993
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                                                                                                                                                100.0%; Fr
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                                                                                                                                                                  1.0%; Score 7; DB 4; Length 461; 00.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7; DB 4; Length 411; Pred. No. 1.2e+02; O; Mismatches O; Indels
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APPLICANT: APPLICANT: APPLICANT:

Vehmaanper , Jari Fagerstr m, Richard Lantto, Raija

APPLICANT:

M ntyl

Arja

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US-08-590-563-8
                                                                   RESULT 22
                                                                                                                                                                                                                                                                    US-08-468-812-8
                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; J
Matches 7; Conservative 0;
             Sequence 8, Application US/08590563 Patent No. 6300114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
PILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
PILING DATE: 29-UUL-1994
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITILE OF INVENTION: Actinomadura Xylanase Sequences and Methods
ITILE OF INVENTION: of Use
                                                                                                                                                        205 LNSDGSV 211
                                                                                                                     447 LNSDGSV 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/468,812 FILING DATE: 06-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paloheimo, Marja
Suominen, Pirkko
Lahtinen, Tarja
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                                                                                                                                                                                                                                                                                                                                       linear
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%; Pred. No. 1.4
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Lynn Dougette-Stamm et al
APPLICANT: Lynn Dougette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCU
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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OTHER INFORMATION: Description of Artificial Sequence: HAP4
US-09-319-989-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.0%; Score 7; DB 4; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                         Query Match 1.0%; Score 7; DB 4; Length 554; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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Patent No. 5882851
GENERAL INFORMATION:
APPLICANT: Koch, Birgit M.
APPLICANT: Sibbeen, Ole
APPLICANT: Halkier, Barbara Ann
APPLICANT: Moller, Birger L.
TITLE OF INVENTION: Cytochrome P-450 Monooxygenages
NUMBER OP SEQUENCES: 24
CORRESPONDENCE ADDRESS:
CURRENT FILING DATE: 1999-06-14

BARLIER APPLICATION WUBBER: PCT/NL97/00688

EARLIER PILING DATE: 1997-12-12

EARLIER PELING DATE: 1997-12-12

EARLIER FILING DATE: 1996-12-12

NUMBER: OF SEQ ID NOS: 9

SEQ ID NO 6

SEQ ID NO 6

LENGTH: 554

TYPE: PRT

ORGANISM: Artificial Sequence
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5569, Application US/09134001C Patent No. 6380370
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US-09-134-001C-5569
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LENGTH: 557
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US-08-656-177A-2
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Batent No. 6190914

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Grivell, Leslie A.

APPLICANT: Teixeira De Mattos, Maarten J.

APPLICANT: Toixeira De Mattos, Maarten J.

APPLICANT: Blom, Jolanda

TITLE OF INVENTION: METHODS FOR MODULATING METABOLIC PATHWAYS OF

TITLE OF INVENTION: METHODS

FILE FERENCE: 24615-22012.00

CURRENT APPLICATION NUMBER: US/09/319,989
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  APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERENE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 4; Length 491;
Pred. No. 1.4e+02;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/32,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: BUGBLSKY, LAWTENCE B.
REGISTRATION NUMBER: 1500
TELERPHONE: 202-311-2600
TELERPHONE: 202-311-2600
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.0
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                       CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                          COUNTRY:
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Query Match
Best Local Similarity
Thes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/656
FILING DATE: 08-AUG-1996
CLASSIFICATION: 800
ATTORNEY_AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/656,177
FILING DATE: 08-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-19783/A/PCT
                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/256,797
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sibbesen, Ole
APPLICANT: Halkier, Barbara Ann
APPLICANT: Moller, Birger L.
TITLE OF INVENTION: Cytochrome P-450 Monooxygenases
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
CLONE: P-450-Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: SOR
                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 558 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                               CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                 USA
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100.0%; Pred. No. 1.
tive 0; Mismatches
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o. 1.5e+02;
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RESULT 28
US-09-347-878-16
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                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Saccharomyces cerevisiae US-09-564-805-240
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                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 240
                                                                                                                     Sequence 16, Application US/09347878C Patent No. 6376210
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                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
APPLICANT: Yuan, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes FILE REFERENCE: 2318-258 CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: pro
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: P-450-Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                     478 EGKTLHK 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100. es 7; Conservative
                                                                                                                                                                                                                                                                                      Local Similarity 100.0%; es 7; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                     EGKTLHK 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Ver.
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Myriad Genetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simard, Jacques
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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100.0%; Pred. No.
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). 1.5e4
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b. 1.8e+02;
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APPLICANT: Toft, Ametre H.
APPLICANT: Marcher, Dorthe
APPLICANT: Pedersen, Hanne H.
APPLICANT: Pedersen, Hanne H.
APPLICANT: Process
TITLE OF INVENTION: Process
TITLE OF INVENTION: Process
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 59283810 No. 5928381disk of No. 5928381th America, Inc. STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: mouse
TISSUE TYPE: brain
PUBLICATION INFORMATION:
AUTHORS: Masayoshi MISHINA
TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 to 1239
                     APPLICATION NUMBER: JP 171155/1992
APPLICATION NUMBER: JP 171155/1992
APPLICATION NUMBER: JP 215017/1992
FILING DATE: J2-AUG-1992
APPLICATION NUMBER: JP 303878/1992
APPLICATION NUMBER: JP 303878/1992
ATTORNEY, AGENT INPORMATION:
NAME: Hamburg, C. Bruce
REGISTRATION NUMBER: 22,389
REFRERENCE/DOCKET NUMBER: F4551
TELECHONE: (212) 986-2340
TELEPHONE: (212) 966-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08687399
Patent No. 5928381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single strand
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
       26-FEB-1992
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NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 008
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US-08-687-399-7
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US-09-405-728-2
i Sequence 2, Application US/09405728
i Sequence 2, Application US/09405728
i Patent No. 6391316
i GENERAL INFORMATION:
i APPLICANT: Potter, Andrew A.
i APPLICANT: Rotux, Clement
i APPLICANT: Rotux, Clement
i TITLE OF INVENTION: CLONING AND EXPRESSION OF HAEMOPHILUS SOMNUS
i TITLE OF INVENTION: TRANSFERRIN-BINDING PROTEINS
i TITLE OF INVENTION: TRANSFERRIN-BINDING PROTEINS
i TITLE NEPREMICE: 9000-0049.20
i CURRENT APPLICATION NUMBER: US/09/405,728
i CRRENT FILING DATE: 1999-09-24
i EARLIER PILING DATE: 1999-03-10
i NUMBER OF SEQ ID NOS: 5
i SOFTWARE: PatentIn Ver. 2.0
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Patent No. 5502166
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
NUMBER OF ENQUENCES:
ADDRESSE:
AD
                                                                                                                                                                                                                                           DB 4; Length 714;
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100.0%; Pred. No. 2.5e+02;
ive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPER. Diskette, 3.50 inch, 1.44 MB storage COMPUTER: 1BM Compatible OPERATING SYSTEM: MS-DOS v.5
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: 26-FEB-1993
                                                                                                                                                                                                               1.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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APPLICATION NUMBER: JP 39563/1992
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LENGTH: 971
TYPE: PRT
CRGANISM: Haemophilus somnus
US-09-405-728-2
                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Lac 7; Conservative
SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 16
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Matches 7; Conservative
                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-09-347-878-16
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ZIP: 951
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US-08-026-138E-3
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; Sequence 4, Application US/08462467B
Patent No. 6210899
; GENERAL INFORMATION:
APPLICANT: Rosenbaum, Jan S
TITLE OF INVENTION: The Use of a BM
TITLE OF INVENTION: Complex for Sc:
TITLE OF INVENTION: Co-Transfected
TITLE OF INVENTION: BMP Receptor
                                                                                                                                                                                                                                                        US-08-462-467B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: DNA (genomic) US-08-687-399-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Beyer, Stefan
APPLICANT: Bloecker, Helmut
APPLICANT: Bloecker, Hera
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Goldberg, Steven L
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Sorangium cellulosum
-09-413-814-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1001 ARGGLAL 1007
                                                                                                                                                                                                                                                                                                                                            673 RGRVMAO 679
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                        ADDRESSEE:
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E: The Procter & Gamble Company
11810 East Miami River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1385 amino acids
                                                                  Rosenbaum, Jan S

VENTION: The Use of a BMP Protein Receptor

VENTION: Complex for Screening Bone Metabolism Actives and Cells

VENTION: Co-Transfected With a Type II BMP Receptor and a Type I
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1.0%; Score 7; DB 4; Le
100.0%; Pred. No. 3.8e+02;
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No. 3.4e+02;
0;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (513) 627-0260 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 54
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 627-0633
                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Hersko, Bart S.
                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                           REGISTRATION NUMBER: 32,572
REFERENCE/DOCKET NUMBER: 54
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: BMP Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 LYARGGL 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: not rele
TOPOLOGY: not relevant
              TELEPHONE: (513) 627-0633
TELEFAX: (513) 627-0260
                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hersko, Bart S
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                       APPLICATION NUMBER: US/08/462,467B
                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                              45061
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                                                                                                                                                                                                                                                                                                                                                                   E: The Procter & Gamble Company
11810 East Miami River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1618 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                USA
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VENTION: The Use of a BMP Protein Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not relevant
                                                                                                                                        435
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complex for Screening Bone Metabolism Actives and Cells Co-Transfected With a Type II BMP Receptor and a Type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.0%; Score 7; DB 100.0%; Pred. No. 3.1 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S.
R: 32,572
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o. 3.9e+02;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
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MOLECULE TYPE: peptide
US-08-159-339A-836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: Bil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6; Conserv
   BENERAL INFORMATION:
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STATE:
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Sequence 8, Application US/08462467B

Patent No. 6210899

GENERAL INFORMATION:

CENERAL INFORMATION:

CENERAL INVENTION:

COMPLEX FOR INVENTION:

TITLE OF INVENTION:

CONTRADECTED WITH A Type II BMP Receptor and a Type I TITLE OF INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCES:

ADDRESSEE: The Procter & Gamble Company

STREET:

STREET:

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SAMPLE COMPANY

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100.0%; Pred. No. 6.6e+02;
iive 0; Mismatches 0; Indels
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ZIP: 45061

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISP PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/462,467B
FILING DATE:
FLING DATE:
FLING DATE:
FLING DATE: BATCH NUMBER: US/08/462,467B
FRISTSTATION NUMBER: 32,572
REFERENCE/POCKET NUMBER: 34.74R
TELECOMMUNICATION NUMBER: 54.74R
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 627-0633
TELEPHONE: (513) 627-063
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2887 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 36
US-08-159-339A-836
; Sequence 836, Application US/08159339A
; Patent No. 6037135
                                                                                   ; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-462-467B-2
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TOPOLOGY: not relevant
MOLECULE TYPE: protein
SEQUENCE CHARACTERISTICS:
LENGTH: 2887 amino acids
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Matches 7; Conservative
                                                                       TYPE: amino acid STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                          405 LYARGGL 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||||
580 LYARGGL 586
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US-08-462-467B-8
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## APPLICANT: Grey, Howard M.

## APPLICANT: Gale Sette A. Heasandro

## CONTINESSES: Towareard and Towaread and Crew Lip

## STATE: A. We Embarcadero Center, Eighth Floor

## CONTINESSES: Towaread and Towaread and Crew Lip

## STATE: A. We Embarcadero Center, Eighth Floor

## APPLICANTON WINDS: 104

## APPLICANTON NUMBER: US/08/150, 139A

## APPLICANTON NUMBER: US/08/150, 139A

## PRINGS PARTE: OG-WAY 1993

## REGORDER TOWARE: US/08/150, 139A

## PRINGS PARTE: US/08/150, 139A

## PRINGS PARTE: US/08/150, 139A

## PRINGS PARTE: US/08/150, 139A

## APPLICANTON NUMBER: US/08/150, 139A

## APPLICANT: Galey Howard M.

## AP
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-159-339A-891
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US-08-191-866D-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5783195
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/191,866D
FILING DATE: 4 February 1994
CLASSIFICATION: 435
CCARSIFICATION: 435
                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 RGPSGL 159
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tes 6; Conser
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                       ZIP: 10036
                                                                                                                                                                                                                                                                  CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 RGPSGL 10
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                                                                                                                                                                                                                                             New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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100.0%; Pred. No. 45;
tive 0; Mismatches
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RESULT 40 PCT-US93-07306-45

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-185-949B-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-191-866D-64
                                 Query Match
Best Local Similarity 100.
Thes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 64,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                               TELEFAX: (212) 278-05
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 391-052
TELEX: 422523
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mark D. Cochran
APPLICANT: Richard D. Macdonald
TITLE OF INVENTION: Recombinant
TITLE OF INVENTION: Rhinotrachei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              472 YKIESG 477
                           472 YKIESG 477
                                                                                                                                                                                                                       ELEPHONE: 1212)
                                                                                                                                                                                                                                                                         NAME: White, John P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 03-NOV CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM 330
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036
                                                                                                                                                                               LENGTH:
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2 YKIESG 7
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New York
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OGY: linear
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)N: 435
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                                                      0.8%; Score 6; DB;
100.0%; Pred. No. 73,
tive 0; Mismatches
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100.0%; Pred. No. 73
ive 0; Mismatches
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                                                                     DB 2;
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                                                                                      Length 17;
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                                                         0; Indels
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GENERAL INFOURMATION:
APPLICANT: McGeer, Patrick L.
APPLICANT: McGeer, Patrick L.
APPLICANT: Rothenberger, Sylvia
APPLICANT: Rothenberger, Sylvia
APPLICANT: Rothenberger, Sylvia
APPLICANT: Wandad Tateuo
APPLICANT: Wennard, Malcolm
TITLE OF INVENTION: Use of psy and Iron Binding Proteins
TITLE OF INVENTION: Use of psy and Therapeutic Agents
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEB: Berselin & Parr
STREET: 40 King Street West
CITY: Toronto
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/285,040
PILING DATE: 01-APR-1999
CLASSIFICATION NUMBER: US/09/285,040
PILING DATE: 01-APR-1999
CLASSIFICATION NUMBER: 40,261
REFERENCE/OCKER TUMBER: 7685-032
TREERENCE/OCKER TUMBER: 7685-032
TREERENCE/OCKER TUMBER: 7685-032
TREERENCE/OCKER TUMBER: 7685-032
TREERENCE/OCKER TUMBER: 7685-032
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 31, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Shona S: McDiarmid
REGISTRATION NUMBER: 38,798
RESTRENCE/DOCKET NUMBER: 7685-006
TELECOMMUNICATION INFORMATION:
TELEPAN: 416-364-7311
TELEPAN: 416-364-7311
TELEPK: 66-23115
TELEPK: 66-23115
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TURE OF THE OF TH
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100.0%; Pred. No. 80;
ive 0; Mismatches
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TELEFAX: 416-361-1398
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 6; Conservative
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TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-520-933-2
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                                Sequence 45, Application PC/TUS9307306
GENERAL INFORMATION:
APPLICANT: MARGOLIS, Richard U.
APPLICANT: RAUCH, Uwe
APPLICANT: MARGOLIS, Renee K.
TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: LOOKING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: LOOKING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: LOOKING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: LOOKING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
ANDREAS OF SEQUENCES: 48
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APPLICANT: Jefferies, Wilfred A.
APPLICANT: McGeer, Parrick L.
APPLICANT: Rothenberger, Sylvia
APPLICANT: Rothenberger, Sylvia
APPLICANT: Food, Michael R.
APPLICANT: Yamada, Tatsuo
APPLICANT: Food, Michael R.
APPLICANT: Kennard, Malcolm
TITLE OF INVENTION: Use of p97 and Iron Binding Proteins
TITLE OF INVENTION: as Diagnostic and Therapeutic Agents
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereekin & Parr
STREET: 40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: 419 SEVERICIA SLIERE, N.W.
CUCUTRY: U.S.A.
ZIP: D.C.
COMPUTER: FLORM:
MEDIUM TYPE: FLORM:
MEDIUM TYPE: FLORM:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
SOFTWARE: PACENTIN Release #1.0, Version #1.25
ATOMORAND NUMBER: PCT/US93/07306
FILING DATE: 03-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,911
FILING DATE: 03-AUG-1992
ATOMNEY/AGENT INPORMATION:
NAME: TOWNSEND GUN K.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MATGOLIS=1A PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 202-137-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

0.8%; Score 6; DB 9
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-520-933-2; Sequence 2, Application US/08520933; Patent No. 5981194
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INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
FRNGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
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COMPUTER READABLE FORM:
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STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 SDGSVR 212
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RESULT 44
US-08-834-130A-59
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Sequence 59, Application US/08834130A PALENT NO. 6.180758
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: GILLAM, Shirley
APPLICANT: OU, Dawei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 59, Application US/08256747C Patent No. 6037448
                                                                                                                                                                                                           Matches
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Matches 6; Conserva
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APPLICANT: CHONG, Pele
                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION USON DATA:
APPLICATION USON DATA:
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TINGLE, Aubrey
TITLE OF INVENTION: SYNTHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 MRGPSG 158
                                                                                                                                                                              22 SSSVFA 27
                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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6th Floor 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                              23 amino acids
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                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canada
                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNTHETIC PEPTIDES FOR A RUBELLA VACCINE
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100.0%; Pred. No.
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100.0%; Pred. No.
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RESULT 45
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 118, Application US/08726306A
Patent No. 5958684
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: 14-
                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                         APPLICATION NUMBER: US/08/726,306A FILING DATE: 02-Oct-1996 PRIOR APPLICATION DATA: GB 95/20080.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 1038-686 MIS:jb
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 14-APR-19:
CLASSIFICATION: 530
                                                                                                           CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                FILING DATE: 02-Oct-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Grosveld, Franklin G.
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US 60/009,832
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Maximum Match 100%
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3776
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Copyright (c) 1993 - 2002 Compugen Ltd.
                                           sp_rodent:*
sp_virus:*
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sp_phage:*
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sp_bacteria:*
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SUMMARIES

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475	479	481	483.5	486.5	486.5	512	656	721	736.5	755	784	788	821.5	832	3244	Score
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Q8yv06 anabaena sp	caulobac	Q8ymk9 anabaena sp	anabaena	Q8yxv8 anabaena sp	Q8ytw7 anabaena sp	Q8yv33 anabaena sp	Q9x6a5 bordetella	Q8zq10 salmonella	Q8x8h4 escherichia	Q8zfy6 yersinia pe	Q9jxu3 neisseria m	Q9jw26 neisseria m	Q51339 pseudomonas	Q9hwl3 pseudomonas	Q9jxz0 neisseria m	Description

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P72599	Q9JTR6	Q8XVB1	Q9EZ93	Q92YC1	8DAX8Ö	Q8YTV3	P72609	9ZUY8Q	806Z8Ö	Q926C6	SDUXBO	086424	Q9F0F9	Q9I422	068599	068590	Q8YTT7	Q8UK13	68IN8Ö	Q93JP3	Q9X7K9.	Q9HUX3	Q8X7W7	Q8YTXS	Q8XR06	P72602	QHYTPO	Q926C7
P72599 synechocyst	Q9jtr6 neisseria m	Q8xvbl ralstonia s	Q9ez93 zymomonas m	Q92yc1 rhizobium m		Q8ytv3 anabaena sp	P72609 synechocyst	Q8yuz6 anabaena sp	Q8z908 salmonella	Q926c6 rhizobium m	Q8yuu5 anabaena sp	O86424 pantoea agg				O68590 pseudomonas			9	Q93jp3 rhizobium l	н		escheric	Q8ytx5 anabaena sp	Q8xr06 ralstonia s	P72602 synechocyst	Q8ytp0 anabaena sp	Q926c7 rhizobium m

ALIGNMENTS

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RESULT 1
Q9JXZ0
ID Q9JX
                                       Query Match
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN=MC58 / SEROGROUP B;

STRAIN=MC58 / SEROGROUP B;

MEDLINE=20175755; PubMed=10710307;

MEDLINE=20175755; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Couperty B.A.,

Cotton M.C., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,

Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,

Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
                                   Receptor; SEQUENCE
                                                             InterPro; IPR002106; AAtRNA_ligaseII.
InterPro; IPR001917; NHtransf 2.
InterPro; IPR001931; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS00599; AA_TRANSFER_CLASS 2; UNKNOWN_1.
PROSITE; PS00339; AA_TRAN_LIGASE_II_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9JXZ0;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                EMBL; AE002532; AAF42164.1; -. TIGR; NMB1829; -.
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NCBI_TaxID=491;
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                                   708 AA; 77068 MW
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                                                                                                                                       DWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFA
                                                                                                                                               EYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA
                                                                                                           FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAA
                                                                                                                   FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRRETFYAAA
                                                                                                                                                                                                IKQKALAFDASYSRPFRLGNTANEFVIGADYNRPRSTNEQGRTTLYARGGLALNEFRSIP
                                                                                                                                                                                                              IKOKAFAVDASYSRPFALGNTANEFVIGADYNRLRSTNEQGRSTL--SKSVALDGFRALP
                                                                                                                                                                                                                                                         TLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYK
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                                                                                                                                                                                                                             QVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKJESGEGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma subdivision; Pseudomonadaceae;
        Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Probable TonB-dependent receptor.
No. 1.4e-182;
smatches 48;
         Mismatches
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 Pred.
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STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
        33;
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Bacteria; Proteobacteria;
         Conservative
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 Local Similarity
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Pseudomonas.
NCBI_TaxID=287;
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Q9HWL3;
01-MAR-2001 (
         627;
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., A. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Waetbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Was A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Raizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."; Nature 406:959-964(2000).

R. BMBL, ABO04333, AAG07555.1; -.
R. Rhal, ABO05331; TonB_boxC.
Pfam, PROD593; TonB_boxC.
Pfam, PROD593; TonB_boxC.
Pfam, PROD593; TonB_boxC.
Pfam, PROD593; TonB_boxC.
R. Receptor, Complete proteome. SIITNQQVKDRNVDTPDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNIDGLPAQMQSI 137 NG---TLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQ 194 Gарв KVGMRYSDRDADSNYAFAG-----SKLGMKTPAGRPG-CNTADDKACAVGLGTEI 361 77 AALSSSVFAAQTADLETVHIKG-QRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIPQSV 217 TQDVISAADLAMFDRVEVVRGATGLMQGAGNPAAAINMVRKRPTQEFRASLQGSVGTWDR 254 YLYQQRHLAP-YNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYG KOKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGL---ALNEFRS 419 IPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGE GKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVG YKGSYMDDRLNARVSFYRMKDKNAA------APLNPNNKKTRYA--ALGKRVMEGVE || : | | : : : : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : TEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDG--IPLLMPKHSANLWTTYQVTPEL--YKAEADVSGSLNSDGSVRGR-VMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAG KLA-----ADKLWARINMLGLYNDCYYSTTGCASMTQNPGDYSYTDDHD------TIGGGVNAMSGI-TSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGG 72; Length 802; Indels Query Match 22.0%; Score 832; DB 16; Best Local Similarity 30.0%; Pred. No. 9.6e-41; Matches 222; Conservative 137; Mismatches 309; ANTFNIPGSERTWTANLRYS 721 GN-LNY-GEPRNLMFTVKYS

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Q51339;
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InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McMorran B.J., Merriman M.E., Rombel I.T., Lamont I.I "Characterisation of the pvdE gene which is required synthesis in Pseudomonas aeruginosa.";
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01-DEC-2001
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Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
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"Nucleotide sequence of pvdD, a pyoverdine biosynthetic gene
Pseudomonas aeruginosa: PvdD has similarity to peptide synthe
J. Bacteriol. 177:252-258(1995).
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Poole K., Neshat S., Krebbs K., Heinrichs D.B.;
"Cloning and nucleotide sequence analysis of the ferripyoverdine receptor gene fpvA of Pseudomonas aeruginosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=PAO;
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                         INPDTVLGAGYLYQQRHL--APYNG-LPA-DANNKLPSLPQHVFVGADWNKFKWNSHDVF
                                                                                                                                                      LTPRETPQSITVVTRQNMDDFGLNNIDDVMRHTPGITVSAYDTDRNNYYARGFSINNFQY 219
LNPDTMLTVGADYQDNDPKGSGWSGSFPLFDSQGNRNDVSRSFNNGAKWSSWEQYTRTVF
                                                 HVELGAGSWDNYRSELDVSGPLTESGNVRGRAVAAYQDKHSFMDHYERKTSVYYGILEFD
                                                                        HAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWD
                                                                                                     DGIPSTARNVGYSAGNTLSDMAIYDRVEVLKGATGLLTGAGSLGATINLIRKKPTHEFKG
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                                                                                                                                                                               ASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNI 127
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Y -> F (IN REF. 1).
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Pred. No. 4.1e-40;
5; Mismatches 312;
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                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis (se
Bacteria; Proteobacteria;
                                                                                                                                               EMBL; AL162753; CAB83866.1; InterPro; IPR000531; TonB_b
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01-DEC-2001 (TrEMBLrel.
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                                                                                                                                                                                       meningitidis Z2491.";
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MTRFKYSLLFAALLPVYAQADVSVSDDPKPQESTELPTITVTADRT-----ASSNDGYTV
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725 AA;
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80302 MW;
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29.9%; Pred. No. 3.2e-38;
cive 117; Mismatches 316
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                                                                              Length
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                                                                                                                                                                                                                                                                             SRHRALNLFAGIEHRFN------QDWKLKAEYDYTRSR--FRQPYGVAGVLSIDH 341
                                                                                                                                                                                                                                                                                                                         KACAVGL---GTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYA 407
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                                                            115 VYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR 174
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STRANDAMS AS SEROGROUP B,
MEDLINE=2018 / SEROGROUP B,
MEDLINE=2017555, PubMed=10710307,
MEDLINE=2017555, PubMed=10710307,
MEDLINE=2017555, PubMed D.W., Peden J.F., Dodson R.J.,
Nelson J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
Cotton M.D., Utterback T.R., Khouri H., Qinn H., Vamathevan J.,
Scarlatco V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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                SGTHTPLGLPMTLREIPQSVSVITSQQMRDQNIKALDRALLQATGTSRQIYGSDRAGYNY
                                                                              KRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQ-TVGASPRPAEKNNRH
                                                                                                                                            | ::|| | | ::|| AELYGILEYDIAPQTRVHAGMDYQQAKETADAPLSYAVYDSQGYATAFGPKDNPATNWAN
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01-0CT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
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TonB-dependent receptor
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                                                                                                                                                                                                                                                                                                                    VYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR 174
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                                                                                                                                                                                                                     MSVFRINMTAATVL-----AALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSS 57
                                                                                                                                                                                                                                                                           SGTHTPLGLPMTLREIPQSVSVITSQQMRDQNIKTLDRALLQATGTSRQIYGSDRAGYNY
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KRLTRKPLFEVRAEAGNRKHFGLDADVSGSLNTEGTLRGRLVSTFGRGDSWRRERSRDA
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'Complete genome sequence of Neisseria meningitidis serogroup
                                                                                                                                            Length 725;
                                                                                                                                         Query Match
20.8%; Score 784; DB 16; Length 7.
Best Local Similarity 29.4%; Pred. No. 5.5e-38;
Matches 228; Conservative 118; Mismatches 320; Indels
                                     EMBL; AE005138; AAF42216.1; -
TIGR; NMB1882; --
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
SECEDTO: Complete proteome.
SEQUENCE 725 AA; 80478 MW; D3953D4485FD8FAF CRC64;
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Science 287:1809-1815(2000)
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P SEQUENCE FROM N.A.

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C STRAIN=CO-92 / BIOVAR ORIENTALIS;

X MEDLINE=21470413; PubMed=11586360;

AA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

AA Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

RA Prentice M.B., Sebaihia M., James K.D., Crucher C., Mungall K.L.,

RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

RA Leather S., Moule S., Oyston P.C.F., Quall M., Rutherford K.,

RA Leather S., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

""monds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
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Best Local Sim
Matches 223;
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InterPro; IPR000531; TonB boxC.
Pfam; PF00593; TonB boxC; 1.
PROSITE; PS01156; TÖNB DEPENDENT REC 2; UNKNOWN 1.
Receptor; Hypothetical protein; Complete proteome.
SEQUENCE 753 AA; 83838 MW; 739512F31D328166 CRC64;
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ARVSFYRMKDKN-----AAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGY
                                                                                                                                                GVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKAS-KTK
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                                                 FVPYSGLTYDINRDLSVYTSYTEIFNPENRRDRNNTLLAPVSGQNYEAGLKGVAFDNSLD
                                                                              FTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLN
                                                                                                                                                                                  LGWNRQRQNIDNDYYLAT-----CNATRTCPDLGDFTQPGWQYPKPVWSDKRAYGSK
                                                                                                                                                                                                                 IGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQV-----
                                                                                                                                                                                                                                                  YPDPQTNIGM-----RPGSLSLIDGA-----RRQQNYDIQVNGQYSLFGRQHQLG
                                                                                                                                                                                                                                                                                 YAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFV
                                                                                                                                                                                                                                                                                                               GRTNYAQSATTASDWASAETRTQTLFSSLQHNFDN-GWNIKGTFTFDNDKLRQDVMWPTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSDRFGFTSRGMAVNNVMRDGVATFYDTRFNYGDNTL-DTDMFDRIEVVRGAAGLMAGPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSN 108
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RESULT 7
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Best Local S
Matches 211
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01-MAR-2002 (TrEMBLrel. 20, L
01-JUN-2002 (TrEMBLrel. 21, L
Outer membrane receptor for f
FHUE OR Z1741 OR ECS1480.
Escherichia coli 0157:H7.
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Q8X8H4;
Q1-MAR-2002
Q1-MAR-2002
Q1-JUN-2002
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino E., Ohnishi M., Murata T., Tanaka M., Tobe T Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
EMBL; AB005320; AAG55848.1; -.
EMBL; AB00533; TonB boxC; I.
                                                                                                                                                                                                                                PROSITE; PS00430; TŌNB DEPENDENT REC 1; 1.
PROSITE; PS01156; TONB DEPENDENT REC 2; UNKNOWN 1.
Receptor; Complete proteome.
SEQUENCE 729 AA; 81231 MW; BBF5ADA133F0595B CR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=0157:H7 / EDL933 / ATCC 700
MEDLINE=21074935; PubMed=11206551;
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                                                                                                                  QFMSVFRINMTAATV-LAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVT
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AGTKMQMTQRDIPQSVTIVSQQRMEDQQLQTLGEVMENTLGISKSQADSDRALYYSRGFQ
                                      VGTKIPASLREIPOSVSIITNOQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYE 121
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                                                                                                                                                        211;
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Last annotation updat
ferric iron uptake.
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Pred. No. 3.4e-35;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
01-EDNOTATION (TrEMBLREL) (Treatment and Pe(III) - ferrioxamine and Pe(III) - rhodotrulic acid uptake.
FHUE OR STM1204.
Salmonella typhimurium.
Bacceria: Prof. 1
EF-GIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNN
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InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   693
                                                                                                                                                                                                                                      293 MNSHDVFADLKHYFGNGGYGKV----GMRYSDRDADSNYAFAGSKLGMKTP-AGRPGCNT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 VTLKORFAESWQATLNATHTEVKFDSKWMYIDALVDKETGTLVSPYGASYPVVGGTGWNS 369
                                                                                                                                                                                                                                                                                       127 IDGLPAQMQS---INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPT-KAFQ 182
                                                                                                                                                                                                                                                                                                                                                     GHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADW 242
                                                                                                                                                                                                                                                                                                                                                                                                                       DINPDIVLGAGYLYQQRHL--APYNGLPA-DANNKLPSLPQHVFVGADW-----NKFK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 DLGTTINLSAGYEYOKIDVNSPTWGGLPRWNTDGSKNSYDRARSTAPDWAYNNKEINKFF 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348 ADDKACAVGLGTE-----IKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 RTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGL 461
                                                                                                                   Gaps
                                                                                                                                                                                                                     67 PASLREIPOSVSIITNOQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYN 126
                                                                                                                                                  13 TAATVLAALSSSV-----FAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 522 ADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAA----APLNPNNKKTRYAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 634 RLPAIPELTVGGGVNWQNRVYKDTTTPYGTFRAEQGSYALVDLFTRYQVTKNFSVQGNIN
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                                                                                   724;
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                                                                                  Query Match 19.1%; Score 721; DB 16; Length 7
Best Local Similarity 27.7%; Pred. No. 2.8e-34;
Matches 208; Conservative 137; Mismatches 321; Indels
                                                94622BFE3714BFC2 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Perric alcaligin siderophore receptor.
PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1; PS01156; TONB_DEPENDENT_REC_2; UNKNOWN_1
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                                 Receptor; Complete profeome.
SEQUENCE 724 AA; 80893 MW;
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                   PROSITE;
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Best Local S
Matches 201
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"Bssential role of the iron-regulated outer membrane receptor FauA:
alcaligin siderophore-mediated iron uptake in Bordetella species.";
J. Bacteriol. 181:5958-5966 (1999).

EMBL; AF135154; AAD26430.1;
InterPro; IPR000531; TonB boxC.
Pfam; PF00593; TonB_boxC; 1.
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DKKYYDQIG
                           NRHYYARVG
                                                         ALHRLTVGGGVDWQSRMYQAAASPRGNVEVEQDSYALVSLMARFDFNKKLSATLNVNNLF
                                                                                                                     V-EGIDLEASGQILEDWNI--GASYTHETTKDASG---NPINTNHERSLEKLYTTYRLEG
                                                                                                                                                  VMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQV--
                                                                                                                                                                                   PIKSKSYELGLKAAYLEGRLNTSAALFQTRQDNLAQVIPGSSIPGFPNMQASR-AASGAK
                                                                                                                                                                                                   PRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAA-----APLNPNNKKTRYAALGKR
                                                                                                                                                                                                                                                SDWKTKOMYFGSRREYRIKNOFTPYAGLTYDINDTYTAYASYTEIFOPONARDTSGGILP
                                                                                                                                                                                                                                                                             GHYKIESGE-GKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLK 528
                                                                                                                                                                                                                                                                                                              ----PAIGSFFDWRRAHIQEPSWADTLSPADDVRTKQTGAYLVGRFALAEPLHLIVGDRW 471
                                                                                                                                                                                                                                                                                                                                           FRSIPOVDLIANARKG---VRGYSHTVATEN---LDEFGIYGKSTFHPADGLSLIGGGRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPAQMQS---INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRETPOSVSVVTROQIEDQGLTDTGAILATAPGISVTRSDSNRYSFSARGFTIDNFQFDG
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                                                                                        -TPELTIGGGVNAMSGITSSAGMHAG-----GYATFDAMAAYRFTPKLKLQINADNIF
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                             700
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27.6%;
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Pred. No. 1.9e-30;
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OS Anaba
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Best Local :
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01-MAR-2002
01-MAR-2002
01-JUN-2002
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InterPro; IPR0005106; AATRNA_ligaseII.
InterPro; IPR000531; TonB boxC.
Pfam; PF00593; TonB boxC; 1.
PROSITE; PS00339; AA TRNA_LIGASE_II_2; UNKNOWN_1.
Receptor; Complete proteome.
Receptor; Complete proteome.
SEQUENCE 863 AA; 95445 MW; 40F9EC04FE462D34 CRC64;
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
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LNARVSFYRMKDKNAAAPLNPNNKKTRYAAL-----GKRVMEGVETEISGAVTPKWQIH
                                                                                                                                          IVTEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVL 106
                                                                                  TKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDR
                                                                                                                      SFDYGPRSSSTERFQTYGIYLQDQITFLDNLKLLIGGRFDWISGENTDNVTGDTTQNPDS
                                                                                                                                                                                         GKFNTGSISHQILIGFDFNHNIDT
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                                                    SAFSPRIGLVYQPSKSVSLYTSYSQSFVPETGVNPDGEIFEPTRGTQYEAGIKADFLEGR
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A., Muraki A.,
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Anabaena sp. (strain PCC 7120)
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Matches 179; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGLPAQMQSING-----TLPNLFAPDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 FOGHAAAGFGTHKQYKAEADVSGSLNSDGSV--RGRVMAQTVGASPRPAEKNNRHETFYA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -AADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-TEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEF 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASLREIPOSVSIITNOQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNI 127
LSATLAAYQITKSNILTP-DPDPER---AALDYLIQVGEQRSRGIELDVAGEILPGWKAI 737
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                                                                  654 GITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERT
                       AGYSYLHSQIKTASNSRDDGIFLL-MPKHSANLWTTYQVTPE----LTIGGG---VNAMS
                                      MEDLINE=21595285; PubMed=11759840; Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., "Complete genomic sequence of the filamentous nitrogen-fixing
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12.9%; Score 486.5; DB 16; Length
Best Local Similarity 24.6%; Pred. No. 2e-20;
Matches 185; Conservative 112; Mismatches 353; Indels
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
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                                                                                                                                                                                                                                                                   630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----QSGDLKGLGFGLGLYYVGDRYADVENTSLLSSYFRTDSALYYKRDNWRLALNFRN 788
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SRDEFTRDIYTLQTEVVGKFKTGSIVHQPLIGVELRR----NTWKYTSFDVADPILLDIF
                                                                                                                                    571 EGFSETASEESLSAFSPRIGIVYQPIQAISLYASYSQSFKPDRFFGRSASNEPFKPTRGT
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                                                                                         RSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHY-KIE
                                                                                                                                                                                                           SGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQT--NLDADGKLLKPRQGN
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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashina K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
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885 AA; 98141 MW; AF7F6BAE0A37FE08 CRC64;
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InterPro; IPR001064; Crystallin.
InterPro; IPR0010531; TonB_boxC.
Pfan; PF00593; TonB_boxC, 1.
PROSITE; P500225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
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MEDIINE=11595285; PubMed=11759840;

Kaneko T. Nakamura Y., Wolk C.P., Kuritz T., Sasamo Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Mur Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yan Yasuda M., Tabata S.;

"Complete genomic sequence of the filamentous nitrog "Coyanobacterium Anabaena sp. strain PCC 7120.";

DNA Res. 8:205-213(2001).
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n; PP00593; TonB boxC; 1.
sptor; Complete proteome.
UENCE 854 AA; 94535 MW; A
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01-MAR-2002
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  MEDLINE=21595285; PubMed=11759840; Kaneko T., Nakamura Y., Wolk C.P., Watanabe A., Iriguchi M., Ishikawa
                                                                                                                       Bacteria; Cyanobac
NCBI_TaxID=103690;
                                                                                                                                                         Anabaena sp. (strain PCC Bacteria; Cyanobacteria;
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4; Mismatches 328;
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  Kuritz T., Sas
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851 AA

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PRELIMINARY;

Q9AC38 Q9AC38; RESULT 15 Q9AC38 ID Q9AC3: AC Q9AC3:

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SEQUENCE FROM N.A.

STRAIN=ATCC 19089 / CB15;

XX MEDLINE=21173698; PubMed=11259647;

XN INCENTANT REGION W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

XX Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

XX Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

XX Detocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

XX Detocka I., Nelson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

XX Olonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

XX Olonay J.F., Smit J., Vanier J.C., Shapiro L., Fraser C.M.;

XX Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

XX Salzberg S.L., Vanie Sequence of Caulobacter crescentus.";

XX TOMPLACE SEGUEN SEQUENCE OF SEQUENCE OF SECUENCE OF SEQUENCE O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHIVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLH------- 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GIKIPASLREIPQSVSIIITNQOVKDRNVDIFDQLARKIPGLRVLSNDDGR---SSVY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 ARGYEYSEYN--IDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRRSFYGVASRDYQKTKSDIATFA-IDHRIDETLNLRQVVRYSKSLNDYIVTNPGDGGAA 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KASKTKFTGY-AGAVYDLNDNNSLYLSLSQLYTP-----QTNLDADGK-----LLKP
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12.7%; Score 479; DB 16; Length 851;
Best Local Similarity 24.7%; Pred. No. 5.8e-20;
Matches 198; Conservative 126; Mismatches 341; Indels 138;
                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
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Pfam: PF00593; TonB_boxC; 1.
Receptor; Complete protecome.
RECURNCE 851 AA; 90124 MW; B75B166237FC5D92 CRC64;
Created)
Last sequence update)
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(TrEMBLrel.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Pfam; PF00593; TonB_boxC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21595285; PubMed=11759840; Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Iriguchi M., Ishikawa A., Kawashima K., Kimura Watanabe A., Iriguchi M., Hishikawa A., Kawashima K., Kimura Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales;
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01-MAR-2002
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        492
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                                                                                                                                                                                                                                                GASPRPAEK----NNRHETFYAAA--DWDINPDTYLGAGYLYQQRHLAPYNGLPADANNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSNDDGRSSVYARGYEY----SEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLF 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVTEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPG-LRV 105
     NA-
                                                FAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIG
                                                                                                                                             PSL----PQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYS----DRDADSNYA
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                                                                                                                                                                                                                                                                                                        FGSGNPGGTINIVTKQPLSEPFYSVEAAIGSYDFYRGAIDLSGPLDDSKTALYR-----L
                                                                                                                                                                                                                                                                                                                                                        DSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTV 220
                                                                                                                                                                                                                                                                                                                                                                                                        ASNYSQFASFTIRGFNSFDQGGNNFTRNGLGYRFGS-QGT--NFSNIERIEVLRGPGSVL
                                                                                                  PNLNGRIPRNRSIGOADSTYSPEIVRVGYNLEHKFSEDWLLRNAFYYSHFYNKTRDTYFA
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176; Conserv
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863 AA; 95343 MW; 3EDA3D64447D2372
LDPDQRTLQRGVQDADDRYQTYDLSTNVVGK---
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25.5%; Pred. No. 1
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Best Local
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Q926C7;
Q1-DEC-2001
01-DEC-2001
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                                                                                                                                                                                                                                            Pfam; PF00593; TonB_boxC;
Complete proteome.
SEQUENCE 733 AA; 79611
                                                                                                                                                                                                                                                                                                  Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591790; CAC46802.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative ferrichrome-iron receptor precursor protein. FHUA1 OR R02223 OR SMC01611. Rhizobium meliloti (Sinorhizobium meliloti). Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
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                                                                                                                                                  MTAATVLAALSSSVFA----AQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIP
AQTGLFLDGLPLFSFGFGNFQVDPFMLERVEVLKGPASVLYGGSNPGGIINLISKRPLDE
                           SEYN--IDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA 180
                                                                                                                      LASGVALAPLMMSGIALAQEGNATQLERIVVEGGNAAGASATGPVDGYVAKATATGSKTA
                                                                                        ASLREIPOSVSIITNOOVKDRN-VDTFDQLARKTPGLRVLS----NDDGRSSVYARGYEY 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA--PLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD
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Last
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509 AATFFNPLVGTGTSDPSDPIN-PAKMVALEPEEGYQYEAGVKYEPSFIDGLLTASVPQIT 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       568 KONVSIAVPGFFVN-----SQLGEVRSRGVELEGKINLNTNWKIISAFSYTDLEVTE 619
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                                                                                                                                                                                                                                                                                                             336 MKTPAGRPGCNTADDKAC-AVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRF 394
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FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKUNRHETFYAAA 240
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                                                                                                                                                                                                                                                                                                                                             241 DWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQ-HV-----FVG----ADWN
                                                                                                                                                    240 SEDLR-----GFILPOVTYAPDDATSLTVFGLLOSLDOVHVGNGFLPYVGTVEDAPFG
                                                                                                                                                                                                        290 KFKMNSHDVFADL------KHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLG
                                                                                                                                                                                                                                                           KIDRDAYYSBPDIDEGSYTQQMLGYEFKHDFDNGWTFTQNARYANLHKHEKYPYTYGYVĞ
                                                                                                                                                                                                                                                                                                                                                                                                               RSTNEQ---GRITLYARGGLALNEFRSIPQ-VDLIANARKGVRGYSHTVATENLDEFGIY
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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Last annotation update)
                                                  PLYYTEVGINSNGNAFTGFDVNDKLNDDGTVRYRLTGKVAGGDN--
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MEDLINE=97061201; PubMed=8905231; Anaka A., Asamizu E., Nakamura Y., Kaneko T., Sato S., Kotani H., Tanaka A., Asamoto S., Kimura T., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Miyajima N., Matosano A., Muraki A., Nakazaki N., Naruo K., Okumura S., Hosouchi T., Matsuno A., Muraki A., Watanabe A., Yamada M., Yasuda M., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                533 NOFEVGYKGSYMDDRINARVSFYRMKDKNAAA----PINPNNKKTRYAALGKRVMEGVE 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              588 TEISGAVTPKWQIHAGYSYLHSQIKTASNSR-DDGIFLLMPKHSANLWTTYQVTPELTIG 646
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                                                                                                                                                                                                                                                                                                   174 RKRP--TKAFQ-GHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEK- 229
TVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA--- 117
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                                                                                                                                                                                              KDFENSËSFIAPVVRLIGNENTNLTASIEYLKYRSFETAP--DLPASGTVISNPNGRVS
                                                                                                                                                                                                                          -DANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDR---DADS
                                                                                                                                                                                                                                            422 RETNLGEPSLSE------SESLVTRL------GY-QLDHRLNDNWTIKSEF
                ----RGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLV
                                                                      256 TPVIRGFESRNLLRNGLRDDSLRFQSEIANV---ERVEVLKGPASVLFGGEDLGGVVNLV
                                                                                                                               --NNRHETFYAAADWDI--NPDTVLGAG--YL-YQQRHLAPYNGLPA------
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Bacteria; Cyanobacteria; Chrococcales; Synechocystis
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EMBL; D90899; BAA16602.1; -. InterPro; IPR000531; TonB_boxC.
Pfam; PF005531; TonB_boxC; 1.
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                                                                                                                                                     NSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG------
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                                                                                                                                                                                                                 RMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLSLTSSSTAIAPENPESEIEVV------ATQEGQGEASYFVPSASTATGLDTPLL 192
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                                                          DNTFVLPSYFRTDAAIFYR-RENWELQLNIENLFNTQYLAE---SNDFDLSVYPGAPFTV
                                                                                      -----GYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNI---
                                                                                                                                                                                                                                                    YQPIPTVSLYGSYTTSFNPSFAASLNADGSTFDPQTGRQFEVGVKAD-ITDKLSVTFSAF
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Best Local Similarity 24.5
Matches 185; Conservative
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EMBL; AL646082; CAD18213.1; -.
InterPro; IPR00531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
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QBXX06; (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN;2002 (TrEMBLrel. 21, Last annotation updat
Probable ferrisiderophore receptor protein.
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STRAIN=GMI1000;
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DGKLLKPRQGNQFEVGYKGSYMDDRLNARVS--FYRMKDKNAAAPLNDNNKKTRYAA-LG
                                               OSRDDLTPKNODLSRTDK-PVSPRLGIVYHPVEALSLYASYSRSFQPLADSFTYYTNSSA
                                                                                                                                                                                LTQQAETFGIRHTLLYGIELGYQDKSDRVAA-----
                                                                                                            VPVVLPTVPANATPSNYGLTHN-----ETYAMYAQDLIKFSPQWTVLAGLR---YEVLK
                                                                                                                                                                                                           IKOKALAFDASYSRPF---RIGHTANEFVIGADYNRFRSTHEQGRTTLYARGGLALHEFRS
                                                                                                                                                                                                                                                                            LKHYFGN-GGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTE
                                                                                                                                                                                                                                                                                                                                                                           EGOKRAEFDLNTSINDDA-----VRARLTGAVEDSGGFRNDYFLRRQAISPSFLFNLSPD
                                                                              ESGEGKT-----LHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTP-----QTNLDA
                                                                                                                                            IPQV--DLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKI--
                                                                                                                                                                                                                                             LDHRINDQWSFHSVVRNYEYALGRNNYVTVSRVTGGAVPTVTLGVNQRNRSDRGTVWQNE
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Receptor; Complete profeome.
SEQUENCE 760 AA; 81956 MW;
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814 GLNFKNIFDVNY
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                           ----LAPQSTTNYEIGAK---YDVSASASVSAALFDMKQTN----LTSVDPATQLAVPIG 545
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                                                                                                                                                              634 WITYQVIPELTIGGGVNA-----MSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQIN
                                                                                                                                                                                       KRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFL-----LMPKHSANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=1195598; bubMed=11759840; MEDLINE=11955985; bubMed=11759840; Marbine=11955985; bubMed=11759840; Maritz T., Sasamoto S., Kaneko T., Nakamara Y., Wolk C.P., Kunitz T., Kaneko T., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Tabata S., Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NOBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor; Complete proteome.
SEQUENCE 851 AA; 93901 MW; 5F93DD9E558D291D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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EMBL, AP003590; BAB74287.1; -
InterPro, IPR00531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12:";
                                                                                                                                                                                                                                                                               707
                                                                                                                                                                                                                     LKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKDNAAAP----LNPNNKKTRYAALGKRV 582
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SEQUENCE FROM N.A.
SETRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkert G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Dimalanta E.T., Potamousis K.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                        583 MEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFL-LMPKHSANLWTTYQVTP
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GLALNEFRS I PQVDL I ANARKGVRGYSHTVATENLDEFGI YGKSTFHPADGLSL I GGGRL
                                        GHYK----IESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKL
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
putative outer membrane receptor for iron transport.
21026 OR ECS0883.
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EMBL; AP002553; BAB34306.1; -.
EMBL; AP002553; DAB34306.1; -.
Plan; PF00593; TonB boxc; 1.
PROSSTE; PS00430; TONB DEPENDENT_REC_1; UNKNOWN_1.
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MEDLINE=21156231; PubMed=11258796;
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Орнихз;
SEQUENCE FROM N.A. STRAIN=ATCC 15692 MEDLINE=20437337;
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01-MAR-2001 (TrEMBLrel. 20, Last
01-MAR-2002 (TrEMBLrel. 20, Last
01-MAR-2002 (Trembrane protein.
                                                      NCBI_TaxID=287;
                                                                                       Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
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 PubMed=10984043;
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9; Mismatches 333;
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SEQUENCE
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MMBL; AB004896; AA608222.1; -. MSSP; P06971; 1BY5.
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InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
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                                                           SLMGVYEFREGWLHGADAGAAVNYVGERAGDSSDSGFELPAYTTVDLLARYPLASNATLG
                                                                                     NLWTTYQVTPELTIGGGVNA-----MSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQ
                                                                                                                   QT----AGEARSQGFDLQFSGQLTEQLRLIGAYAYIDAEVTKDENIARGSRLLNVPKHSG
                                                                                                                                                                                                        YTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKN--AAAPLNPNNK
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Pred. No. 6.7e-19;
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GSPGGLVNKISKLPTEEPIHEVGISYSTKDRAQAMFDFGGPI-SEGN--DDFLYRIVGLA 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 TNEQGRITLYARGGLALNEFRSIPQVDLIANARKGVRG----YSHTVATENLDEFGIYG- 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ------EYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 -RHGDNNFDIADDRYFLAPSFTWKPDEGTSFTLYG---LAQSDETDANVGAITTVDGKIL 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 NITTVGDYRDSLRQPYINYGMFRTD--PYQLQ-------RVEVIKGPVSVLYGS
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Rhizobiaceae, Rhizobium.
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726 AA; 79499 MW; BDEBF2A5CSAA0408 CRC64;
                                                                                                                                           Last sequence update)
Last annotation update)
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llarity 23.8%; Pred. No. 7.9e-19;
Conservative 115; Mismatches 313.
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Pfam; PF00593; TonB boxC; 1.
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Microbiology 146:829-837(2000)
Microbiology 146:829-837(2000)
EMBL; AJ238208; CAB41037.1; --
HSSP; P06971; 10J0.
                                                                                                                01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20,
                                                                        PRELIMINARY;
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STRAIN=8401 PRL1;
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31, Carter R.A.;
"Structure, function and regulation of the Rhizobium leguminosarum vbs "Structure, function and regulation of the Rhizobium leguminosarum vbs genes, which specify the synthesis of the siderophore vicibactin.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ315451; CAC48054.1; -.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC. 260 -RHGDNNFDIADDRYFLAPSFTWKPDEGTSFTLYG---LAQSDETDANVGAITTVDGKIL 315 163 | ||:|| : || || GSPGGLVNKISKLPTEEPIHEVGISYSTKDRAQAMFDFGGPI-SEGN--DDFLYRIVGLA 259 276 SLPQHVFVGADWNKFKWNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGM 336 909 63 GTKIPASLREIPOSVSIITNOOVKDRNVDTFDQLARKTPGLRVLSN--DDGRSSVYARGY 120 157 607 LHSQIKTASNSRDDGIFLLMPKHSANLWTTY---QVTP--ELTIGGGVNAMSGITSSAGM 661 -----GAIDKNYEGLTAAFNIRNIADQRDTVCNEGF 709 Gape 97 PRPAEKN--NRHETFYAAADWDINPD----TVLGAGYLYQQRHLAPYNGLPADANNKLP MTAATVLAALSSSVFAAQTAD----LETVHIKGQRSYNAIVTEKNGDYSSFAV---TV -----EYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSS 158 NITTVGDYRDSERQPYINYGMFRTD--PYOLQ------RVEVIKGPVSVLYGS GEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGAS FTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYM---DD NHSEVTGGDNEGNTPAF - - TPAHVASLWANYTFQETNPFNGLSVGAGVRYVSENWTDTAN 662 HAGGYATF--DAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIP-----547 RINARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWOIHAGYSY Rhizobium leguminosarum (biovar viciae). Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium. Query Match
12.1%; Score 458; DB 2; Length 747;
Best Local Similarity 23.8%; Pred. No. 8.2e-19;
Matches 189; Conservative 115; Mismatches 313; Indels 178; F6FE332B01AB4F92 CRC64; Last sequence update) Last annotation update) 747 AA (TrEMBLrel. 19, Created) PRT; 01-DEC-2001 (TrEMBLrel. 19, Last se 01-MAR-2002 (TrEMBLrel. 20, Last ar Ferric hydroxamate uptake receptor FHUA. 747 AA; 82183 MW; TSKNPSSFYVDASAAYDF----710 CYLGOGRNMTATLKY 724 PRELIMINARY; ---GSERTWTANLRY SEQUENCE FROM N.A. NCBI_TaxID=387; Q93JP3; 01-DEC-2001

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01-JUN-2002
01-JUN-2002
                                                                                                                                       C58.";
Science
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Wood D.W., Setubal J.C., Kaul R., Monke D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Kutyavin T., Levy R., Li M.-J., WcClelland E., Romero P., Gordo
Raymond C., Rouse G., Saenphimmeachak C., Wu Z., Romero P., Gordo
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Kreepan W., Perry
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
Nester P.
MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin
Houmiel K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
                                                                                                                                                                       Nester
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ATU0409 OR AGR C 718.
Agrobacterium tumefaciens
                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                    E.W.,
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Science 294:2323-2328(2001).
EMBL; AE009012; AAL41430.1; ALT_INIT
EMBL; AE007978; AAK86224.1; -.
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Q8UK13; Q8UK13; 01-JUN-2002 01-JUN-2002 01-JUN-2002

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MEDLINE-21608551; PubMed=11743194;
MEDLINE-21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Houmiel C., Allinger M., Doughty D., Scott C., Lappas A.,
Flanagan C., Allinger M., Gurson J., Lomo C., Sear C., Strub G.,
Flanagan C., Stater S.;
Cielo C., Slater S.;
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                                                                                        Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
11.9%; Score 450; DB 16; Length 819;
Best Local Similarity 25.5%; Pred. No. 2.8e-18;
Matches 187; Conservative 106; Mismatches 349; Indels 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89022 MW; 976C509F6DE91628 CRC64;
                     Agrobacterium Tume Faciens (strain C58 / ATCC 33970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE0008953; AAL45999.1; --
EMBL; AE007900; AAK80685.1; --
Plasmid, Receptor; Complete profeome.
SEQUENCE 819 AA; 89022 MW; 976C50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 294:2317-2323(2001)
                                                                                                                                   Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
ATU5311 OR AGR PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nester E.W.;
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                                                                                       574 KIDTAFTGRAGLIYLFDNGFAPYVSYSTSFMPYSGFDGQNNPFKPTTGEQWEVGLKYEPV 633
                                                                                                                                                                                                         634 GYDALITVSAFDLKQKNV-----PTYDEFTYLPAQTGEIHVQGIEIEGKATVFDSLDLIA 688
                                                                                                                                                                                                                                                                                          657
                                                                                                                                                                                                                                                                                                                                                                                                      SA-GMHAGGYATFDAMAAYRF---TPK---LKLQINADNIFNRHYYARVGGANTFN--IP 708
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
522 PTVGARW-----DNRISQLGLYAQDQI-KWDNWILTLGGRY-DWALQTDNDILSSTIGK 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaneko T. Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Mateumoto M., Mateuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., A Yasuda M., Tabata S., "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium mabaena sp. strain PCC 7120.";

In DNA Res. 8:205-213 (2001) -.

REMBL; AP003590; BAB74325.1; -.

RINTERPO; IPR001484; Pyrokinin.

RINTERPO; IPR000531; TonB boxC; 1.

R Pfam; PF00593; TonB boxC; 1.

R PROSITE; PS00599; PYROKININ; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                           485 ASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPROGNQFEVGYKGSYM
                                                                                                                                                                        545 DDRLNARVSFYRMKDKNAAAPLNPNNKKTRY--AALGKRVMEGVETEISGAVTPKWQIHA
                                                                                                                                                                                                                                                                                       GYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQV----TPELTIGGGV-NAMSGITS
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Bacteria, Cyanobacteria, Nostocales; Nostocaceae; Nostoc
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SEQUENCE 872 AA; 95972 MW; 6485E569DBEA3E61 CRC64;
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Last annotation update)
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O68590;
O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 07, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYDROXAMATE-type ferrisiderophore receptor (Iron transport protein
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

MEDLINE=9621057; PubMed=8633080;

Ochsner U.A., Vasil M.L.;

"Gene repression by the ferric uptake regulator in Paeruginosa: cycle selection of iron-regulated genes.

Proc. Natl. Acad. Sci. U.S.A. 93:4409-4414(1996).
                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAO1;
Ochsner U.A., Vasil A.I.,
Submitted (MAR-1998) to the
                                                 Pseudomonas aeruginosa compared Submitted (JUN-2000) to the EMBI
SEQUENCE
                              TRYCHAIR ROOM TO THE PROOF L. L.;
Schwan W.R., Barker L., Brody L.L.;
Schwan W.R., Barker L., Brody L.L.;
"Differences in sensitivity to PA-1806 among iron transport
"Besudomonas aeruginosa compared to Escherichia coli.";
Pseudomonas aeruginosa compared to Escherichia coli.";
Pseudomonas aeruginosa compared to Escherichia coli.";
                                                                                                                              Schwan W.R.,
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
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he EMBL/GenBank/DDBJ
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Best Local :
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EMBL; AP051690; AAC06215.1; --

EMBL; AP276976; AARP07743.1; --

EMBL; AE004865; AAR077902.1; --

InterPro; IPR000531; TonB boxC; T.

Pfam; PF00593; TonB boxC; T.

Receptor; Complete proteome.

Receptor; Complete proteome.

SEQUENCE 753 AA; 82336 MW; 4DD5430DC9D6514B CRC64;
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MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                    635
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|:::||| |:| ||:| ||:| ||:| || ||
DGEQRVQGVELGFNGKLTEKWKVFGGYTYLDSEIRKSTVKSDEG--NKMPQTAQNNFTLW
TTYQVTPELTIGGG---VNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIF
                                                                                                                                                                                                                                                                                                                                     QKALAFDASYSRPFRL-----
                                                                                                                ADISVGNNGLDPERNRNLELGTKWAFFDDALSLNAALFR-TDKTNARVASP-DVSTLQVL
                                                                                                                                               TNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAA
                                                                                                                                                                                  GPAGYFKRE-----NNSHFWNYQTGLVYKPAPNGSIYLAWSTSSNPTGETGGEGQ
                                                                                                                                                                                                                   GRLGHYKIESGEGKTLHKASKTKFTGY-AGAVYDLNDNNSLYLSLSQLYTP------
                                                                                                                                                                                                                                                  TDTKTSAAYVFDTLKLSEQWELNLGLR------YDDFDT--KSSGYQTAGRN----
                                                                                                                                                                                                                                                                                     FRSIPQVDLIANARK----
                                                                                                                                                                                                                                                                                                                    --EFSYEDVHNRPYAITSGGGAGNTCNARLLASGDCTSLNRPTPGDNWTGSITDGLAYTD
                                                                                                                                                                                                                                                                                                                                                                                       NVANGYVYRSAKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSS----VYARGY
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22.9%;
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                                                                                                                                                                                                                                                                                 -GVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGG
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Pred. No. 7.
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TTYDLLQNFTIGGGTTYVDKQYGNTANS-TYIPSYWRYDAMASYKVSKNVDLQLNVQNLT 723
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"Gene repression by the ferric uptake regulator in Pseudomonas aeruginosa: cycle selection of iron-regulated genes.";
proc. Natl. Acad. Sci. U.S.A. 93:4409-4414(1996).
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Ochsmer U.A., Vasil A.I., Johnson Z., Vasil M.L.;
Genetic characterization of novel siderophore receptor (a rom acquisition in Pseudomonas aeruginosa.";
in iron acquisition in Pseudomonas aeruginosa.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR055693; AAC06225.1;
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Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; UNKNOWN_1.
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PFUA.
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MEDLINE=96210657; PubMed=8633080;
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                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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SEQUENCE
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127 IDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAA 186
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STRAIN=ATCC 15692 / PAO1;

STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Colt., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Colt., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Broder R.L., Goulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Brody L.L., Coulter S.N., Folger K.R., Wu Z., Paulsen I.T., Spencer D.H., Wong G.K.-S, Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
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                                                                                                                                                                                     KTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTN-----LDADGKLLKPRQGNQFEV 537
                                                                                                                                                                                                                                                                                    597
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                                                                                                                                                                                                                                                                                                             538 GYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPK
                                                                                                                                                                                                                                                                                                                                                                            WQIHAGYSYLHŞQIKTASNSRDDGIFL-LMPKHSANLWTTYQVTPELTIGGGVNAMS--G
                                                                                                                                                                                                                            404 KFYPANGFDLHNPPGYWNGPTDKRDSARNRTELEVKALYAFDTIALDE-----RWDLSLG
                                                                                                                                      459 LRYDWIDGTSRSTPS------GKPT--------VRADSSDG-----
                                                                                          428 AR-KGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKAS
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Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Nature 406:959-964(2000).
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC: 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; UNKNOWN_1.
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequel-OCT-2001 (TrEMBLrel. 18, Last annuprobable TonB-dependent receptor.
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SEQUENCE 732 AA; 80835 MW;
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Query Match
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Matches 179;
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-21064758; PubMed=11136137;
Medlindo M.A., Day W.A., Raphael B.H.,
Galindo M.A., Day W.A. Raphael Ca
"Cloning and Characterization of a Ca
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
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NCBI_TaxID=197;
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                                                                                                                                             Microbiol. 42:139-143(2001)
AF241226; AAG47637.1; -.
P06971; 1BY5.
Pro; IPR000531; TonB_boxC.
PF00593; TonB_boxC; 1.
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     Conservative
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                                                                                                 83851 MW;
11.4%; Sc
23.9%; Pr
tive 116;
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Score 432; DB
Pred. No. 2.8e
16; Mismatches
                                                                                                 C4140C3D258202E0 CRC64;
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    Joens L.A.;
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                       DB 2;
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01-NOV-1998
01-DEC-2001
MEDLINE=98348446; PubMed=9683481; Killmann H., Herrmann C., Wolff H. "Identification of a new site for
                                        STRAIN=K4
                                                                           NCBI_TaxID=549;
                                                                                                                                              Ferrichrome
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                                                                                                      Bacteria;
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                                                                                                                                                                                                                                                                                                                                                      GIFLL-MPKHSANLWTTYQ----VTPELTIGGGVN-----
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                                                                                                      agglomerans.
a; Proteobacteria;
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                                                                                                                                                                                                        77 VSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVY----ARGYEYSEYN--IDGL 130
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                                                                                                                                                                                                                                                                                                                                                                                        302 LKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEI 361
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                                                                                                                                                           20 ALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAV---TVGTKIPASLREIPQS
                                                                                                                                                                                                                                                     PAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFG
                                                                                                                                                                                                                                                                                                  191 THKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                     KOKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                    528 KPRQGNQFEVGYKGSYMDDRLNARVSFYRM-KDKNAAAPLNPNNKKTRYAALGKRVMEGV
 'n
                                                                                                                                       94;
  coli, Salmonella paratyphi
                                                                                                                Length 732;
                                                                                                              Query Match
11.4%; Score 429; DB 2; Length 73
Best Local Similarity 23.7%; Pred. No. 4.1e-17;
Matches 172; Conservative 105; Mismatches 356; Indels
                                                                                          732 AA; 80897 MW; 8706DFAA883BC190 CRC64;
         Salmonella typhimurium, and Pantoea agglomerans."; J. Bacteriol. 180:3845-3852 (1998).
EMBL; Y14026; CAA74355.1; -. HSSP; P06971; 1BY5.
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Last sequence update)
  FhuA proteins of Escherichia
                                                       InterPro; IPR000531; TonB boxC. Pfam; PF00593; TonB boxC; 1. Receptor. 732 AA; 80897 MW;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
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QBYUU5
ID QBYUU
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DT 01-MA
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VNNRLVGV----PYNSASLWTTYELQQGNLQGLGLGLGGVVYVGEREASLPNNLKIPSYVR 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 SNDDGRSS--VYARGYEYS-EYNIDGL-----PAQMQSINGTLPNLFAFDRVEVMRGP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 IVTEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVL 106
                                                                                                                                                                                                                                         MEDLINE-2159528; PubMed=11759840; Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Walk Caneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yamada M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Yamobacterium Anabaena sp. strain PCC 7120."; LOmplete genomic sequence of the filamentous nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120."; EMBL, AP003588; BAB73951.; ... REMBL, AP003588; BAB73951.; ... RINTERPRO, IPR001484; Pyrokinin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNNSLYLSLSQLYTPQT-NLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLP-SLPQHVFVG-ADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 -SGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRV
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11.2%; Score 424; DB 16; Length 8
Best Local Similarity 23.8%; Pred. No. 1e-16;
Matches 170; Conservative 124; Mismatches 328; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEAM; PF00593; TONB'boxC, 1.
PROSITE; PS00539; PYROKININ; UNKNOWN 1.
Receptor; Complete protecom, 93AA9B341C8C5003 CRC64;
11-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                             Anabaena sp. (strain PCC 7120).
Bacteria: Cyanobacteria; Nostocales; Nostocaceae;
NCBI_TaxID=103690;
                                Ferrichrome-iron receptor.
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Q926C6
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Best Local :
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01-DEC-2001
01-DEC-2001
01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000531; TonB_boxC.
Pfam; PF00553; TonB_boxC; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21396507; PubMed=11481430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative ferrichrome-iron receptor precursor FHUA2 OR R02269 OR SMC01657.
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      LDGRGVSPPLDTKNPTQGRPVDAIDF--
                                                     EQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPA
                                                                                                                                                                                                                                                                                           HVFVG-ADWNKFKWNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVM-----AQTVGASPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRV--LSNDDGRSSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDASIFYK-RUNWRAALNFKNLFDTKYYE---SQSFFIVPAAPFTVLGTVSFEF
                                                                                                                                                                                                                                         DIFAGNEDENDSVQKQGRVGYEFEHRLNDTEVERQNARVSTLNIDADWAFAYAP-----
                                                                                                                                                                                                                                                                                                                                                                                                                      PAEKNNRHETFYAAADWDINPD----TVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITKRPTEDTLREVQVQYGSHDRYQGQFDFSGPVNENDPVYYRLTGLLRDADTEQVGLADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRGFDVTYSGVFRDNLRQPAAVDSIFKNEP--YGLEGVSILRGPSSALYGATGAGGLYNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARGYE--YSEYNIDGL--PAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSATGAKIDTPFLETPQSISTVTEQQLKDRNPQTLLETLAYTPGTRVGAYGFDPRFDAFF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPLIRLALAGTSALALVATA--QAQEAEQETVSNGDSTALETLVVNGSGGVITAEGYVGT
                                                                                                                                                                             AGRPGCNTADDKACAVGLGT-EIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTN
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Pred. No. 9e-17;
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InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
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                        235 TFYAAADWDINPDTVLG-AGYLYQ------QRHLAPYNGLPADANNKLPSLPQH 281
                                                                        VFVGA-DWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPA 340
                                                                                         Gape
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                                                                                                                                        DGLSLIGGGRLGHYKIESGECKTLHKA----SKTKFTGYAGAVYDLNDNNSLYLSLSQLY
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MEDLINES-2185-2818; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Kimura T.,
Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Natsumo A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
Tompleter genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabana sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
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llarity 23.1%; Pred. No. 1.6e-16;
Conservative 117; Mismatches 327; Indels 177;
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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InterPro, IPR00531; TonB boxC.
Pfam, PR0559; TonB boxC; 1.
SECEPTOR; Complete proteome.
SEQUENCE 853 AA; 94548 MW; 67EA77C09E049437 CRC64;
                                                222 ALMPSLTWRITDRTRLDLMAYLHRDPQGGSHSGLPYQGTVVPYNG----
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Last annotation update)
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01-MAR-2002 (
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| : | : | : | | | | : | : | 194
                                                                                                                                                                                                                                                                                                        VLSNDDGRSSVYARGYEYSEYNI -- DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDS 162
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MEDLINE-97061201; Pubmed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
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                                                                                                                           46 AIVT-EKNGDYSSFAVTVGTKIPASLREIPOSVSIITNQQVKDRNVDTFDQLARKTPGLR
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
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Best Local Similarity 23.2%; Pred. No. 2.7e-16;
Matches 178; Conservative 116; Mismatches 311
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InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS00539; PYROKININ; UNKNOWN_1.
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                                                                                                                                                          VSFYRMKDKNAAA--PLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHS 609
DLNNSFQIPSYLRTDI---SVFYRRNNWRAAINVNNLFNIDYIEAT
                         DAMAAYRFTPKLKLQINADNIFNR--HYYARVGGANTFNIPGSERT 713
                                                               RVTKDDNLEPGNLLEGVPFNSASLWSTYEIQ-----AGDLQGLGFGLGLFYVGERQG 788
                                                                                              QIKTASNSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATF 669
                                                                                                                                   LAAYEITVSNLAVTDPENPNFS----IPSGEQRSKGVEFDIAGEILPGWNIIASYAYTDA 736
                                                                                                                                                                                                          PRLGIVYOPIEPVŚLYASFSRSFOPNFGTRFDGSLLEPVFGTQYEVGVRGEFLDGRLIAN 680
                                                                                                                                                                                                                                GYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNAR 551
                                                                                                                                                                                                                                                                              NDFPDVFSSEGQTNTLG1FLQDQVTLTDNLKLLMGGRFDT1DQSSSSNGESDERYDQAFS
                                                                                                                                                                                                                                                                                                                RGYSHTVATE-NLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFT 491
                                                                                                                                                                                                                                                                                                                                                   ---KF-STGPIQHTLLFGVDLSWQSAPFIFRGGVA-----APTINIFNPVYGTVARPSI 560
                                                                                                                                                                                                                                                                                                                                                                                   DYNRFRSTNEQGRTTLYA------RGGLALNEFRSIPQVDLI-----ANARKGV 432
                                                                                                                                                                                                                                                                                                                                                                                                                          DNWK----LRNRFRFSYLDQAAEQTELVKLDETTGNLSRQFSRNEQQIRNYELQTDLIG- 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDKACAVGLGTEIKQKALAFDASYSRPFRL----GNTANEF------VIGA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MNSHDVFADLKHYFGNG----GYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISPVVTWQISDQTDLRFEWDYLYDRR---PFDRGIVA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FYAAADWDINEDTVLGA--GYLYQQRHLAPYN-GLPADANNKLPSLPQHVFVGADWNKFK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G----FQQFGGTLRDGFKFRDNFSIPDTANLQRIEVLKGPASVLYGNLDPGGVINYITKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNATDQSLVLGLSPGKGVADEED------GNDAIQVVVTGEQDEGYAVDDATTATLTDT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLSEPFYEVAMOAGNFGLVRPTIDLSGPLNSORTALYRLNAAYEGGGNFRDFDTEVARFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLPAQMQSINGTLPNLFAF------DRVEVMRGPSGLFDSSGEMGGIVNLVRKR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLRDIPQSIQVVPQQVLEDRQIIRASEALQNVSGVQRGNTVGGTSEI-----FNIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------FGTGIADIPFDRVLGELDDFDARTNFS-AGYRLEHR-----FS 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRV-MAQTVGASPRPAEKNNRHET 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNID 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            853 AA; 94170 MW; 11369D592F1F9D9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 116; Mismatches 311; Indels 161; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         418
                                                                                                                                                                                                                                                                                620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
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מא כ	RESULT 39	
HK	ID Q8YTV3	PRELIMINARY; PRT; 857 AA.
Ų.	AC Q8YTV3; DT 01-MAR-2002	(TrEMBLrel. 20, Created)
āā	DT 01-MAR-2002 DT 01-JUN-2002	(TrEMBLrel. 20, Last se
9 D	errichrome	iron receptor.
00	OS Anabaena sp	(strain PCC 7120).
100	OC Bacteria; Cyanoba OX NCBI_TaxID=103690	cteria; Nosto
본	RP SEQUENCE FR	OM N.A.
יק יק	RX MEDLINE=215	Kuritz T Cagamoto G
ן יש ו	Watanabe A.	A., Kawashima K., Ki
면 전	RA Kishida Y., RA Nakazaki N.	, Matsuno A., Muraki A., , Takazawa M., Yamada M.,
יק נ	RA Yasuda M.,	
z z	RT "Complete g RT cyanobacter	"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
! 22!	RL DNA Res. 8:	01).
	OR EMBL; AP003590; BAB74: OR InterPro; IPR000531;	590; BAB74309.1; PR000531; TonB_boxC.
ខ្ល	W Receptor; C	oteome.
9		1000 km, 1010000000
	Best Local Sim Matches 174;	Similarity 23.6%; Pred. No. 3.2e-16; 2007. 4; Conservative 106; Mismatches 296; Indels 161; Gaps 28;
γQ	47	GDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVL 106
뫄	204	VVTGQQDRYSVPNATTATRTDTPLRDIPQSIQAVPRQVLEDRQVIRASDALRSVSGVQQG 263
Ş	107	PAQMQSINGTLPNLF
В	b 264 NKVGGTS	SEVFNIRGFPQFGGNLRDGFNNRNNFSIVETANLERIEVLK 310
Ş	155	GPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR 212
ДD	311	- ;
Q.	213	GRVMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYN-G 266
닭	b 369 YRLNA	AYERGGNFRNFDTEVERFFISPVVTWKIGDRTDLRLELEY-SNDKRPYDRG 423
8	267	ADWNKFKMNSHDVFA
뫄	b 424 LVAFGTG-	3-IADIPFDRVLGEPDDFSERTNFLAGYRLEHRFNDDWKLRNQFR 473
S	318	NYAFAGSKLGM
밁	474 YSSSI	QTNNRLEPGRINETIGE
Ş	378 LGN-	LNEFRSIPOV
밁	502 LGEF	TVRNYELQTDLVGNFATGSIQHTLLFGVDLSWVNDGGVSLFEPAPSIN-IFNPV 558
δ.	430	KGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIES 476
дb	b 559 YGI	ATRPSRDEFADVFPFGSQTDSIGVFVQNQITLAENLKLLVGGRFDNIDQSS 612
Ş	477 GE	KASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFE 536
ДD	613 AS	DERQDQAFSPRVGIVYQPIEPISLYTSFSRSFQPNFGNRADGSLLEPVRGTQYE 668
ĮŞ	537 VGYKGS	LNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISGA
밁	669 VGVRGE	FLNGSLITNLAAYEITRSNLAVTDPDNPNFSIPSGEORSRGVELDVTGOI 724

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 VEHQLGSGWKVDAGLSYRTSRLFGKSSDASRLLDDGRTLWRQARERD--YHANDLAGRVD 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 LGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEF 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 MQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 ITNOQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA-RGY-----EYSEYNIDGLPAQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 VṛRAALDGFGATRLDTALDWVSGISRQNNLGGIADNFAIRĠFAGDLNTGSDYLVNĠFSA- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 ALSSSYFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIPQSVSI 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                              ---YATFDAMAAYRFTPKLKLQINADNIFNRHYYA--- 697
                                                                                                                         - DIVLGAGYLYQQRHL-APYNGLPADANNKLPSLPQHVFVGADWN---KFRMNSHDVFAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDINP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salanoubar M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottler P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siquier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A., Weissenbach J., Boucher C.A., Gonome sequence of the plant pathogen Ralstonia solanacearum.";
TPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, beta subdivision, Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6E9BBAFCDBD092C5 CRC64;
                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Putative ferrichrome-iron receptor protein.
RSC2729 OR RS00125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
10.9%; Score 412; UB 10; 1885; Pred. No. 3.7e-16;
Best Local Similarity 22.8%; Pred. No. 3.7e-16;
Matches 170; Conservative 127; Mismatches 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.9%; Score 412; DB 16; 22.8%; Pred. No. 3.7e-16;
                                                                                                                                                                                                                                                                                                                                                                         689 AA
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL646071; CAD16436.1; -...
InterPro; IPR000531; TonB boxC.
Pfam; PF0053; TonB boxC; 1.
Complete proteome:
SEQUENCE 689 AA; 74213 MW;
                                                                                                                                                                                                        698 ----RVGGANTFNIPGS 710
                                                                                                                                                                                                                                                    836 ORRNRINPGEPFTVRGT 852
                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 415:497-502(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                 655 ITSSAGMHAGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=GMI1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ralstonia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247
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A Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

A Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,

RA Barloy-Hubler F., Bowser L., Hyman R.W., Kahn D., Kahn M.L.,

RA Kalman S., Keating D.H., Palm C., Surzycki R., Wells D.H.,

RA Yeh K.-C., Davis R.W., Federapici N.A., Long S.R.;

A York C., Davis R.W., Federapici N.A., Long S.R.;

Rinchizotide sequence and predicted functions of the entire

RT Sinorhizotium melliloti pSymA megaplasmid ";

Rinchizotium melliloti pSymA megaplasmid ";

Rocci Natl. Acod. Sci. U.S.A. 98:9883-9888(2001).

R Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).

R Proc. Natl. Acod. Sci. U.S.A. 98:9883-9888(2001).

R Receptor; Plasmid; Hypothetical protein; Complete proteome.

W SEQUENCE 714 AA; 78235 MW; 4DABSF4862934A69 CRC64;
 122 YSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAF 181
 65 -KIPASLREIPQSYSIITNQQVKDRNVDTFDQLARKTPGL--RVLSNDDGRSSVYARGYE 121
 Gaps
 64
 24 LLGCTAFFALTPALSFAQDAVPEGDTTVLETIVAHGAGGGSVLNTDEDSKSIIATETTGA 83
 643 LTIGGG---VNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARV 699
 587
 588 TEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLL-MPKHSANLWTTYQV----TPE 642
 664
 432
 471
12 MTAATVLAALSSSVFAAQ-----TADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGT
 417 RSI-----PQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGH
 385 DPVYGQPRPALRPSSSTRESORG------FGAFVQDQVTLTPQWKLLAGVRMDR
 530 ROGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAA--PLNPNNKKTRYAALGKRVMEGVE
 472 YKIESGEGKTLHKAS--KTKFTGYAGAVYDLNDNNSLYLSLSQLYTPOTNLDADGKLLKP
 Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.
 Query Match
10.9%; Score 411; DB 16; Length 714;
Best Local Similarity 24.6%; Pred. No. 4.5e-16;
Matches 187; Conservative 110; Mismatches 344; Indels 120;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 Putative ferrichrome-iron receptor.
RA0963 OR SMA1747.
Rhizobium meliloti (Sinorhizobium meliloti)
 714 AA.
 700 GGANTFN----IPGSERTWTANLRYSF 722
 665 -- ASSYNELWVAPCAEROVTLAATYTF 689
 PRT;
 MEDLINE=21396509; PubMed=11481432;
 PRELIMINARY;
 [1]
SEQUENCE FROM N.A.
 340 LOGEV-
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STRAIN=ZM4;

Shin I.S., Kang H.S.;

EMBL; AR300471; AAG42412.1; -.

HSSP; P06971; 1QJQ.

InterPro; IPR001899; Gram pos anchor.

InterPro; IPR001831; TonB boxC.

Pfam; PF00593; TonB boxC; 1.

PFam; PF00593; TonB boxC; 1.

PROSSITE; PS00343; GRAM POS ANCHORING; UNKNOWN 1.
 Q9EZ93;
 SEQUENCE
 SEQUENCE FROM N.A.
 Zymomonas mobilis.
Bacteria; Proteoba
 01-DEC-2001 (TrEMBLrel. 19 Ferrichrome-iron receptor
 01-MAR-2001
01-MAR-2001
 NCBI_TaxID=542;
 Zymomonas
 513
 677
 683
 619
 567
 572
 519
 458
 464
 404
 406
 352
 349
 308
 289
 251
 182
 144
 42
 Match
 LQINADNIFN-RHYYARVGGANTFNIPGSERTWTANLRYSF
 KVRH------RGFELEAKAEVTNNISVIAAYSYIDSKIEEPGGANDGNRLMRVPKNMA
 KTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSA
 NLDADGKLLKPRQGNQFEVGYKGSYMDDRLNA--RVSFYRMKDKN----AAAPLNPNNK
 IGGGR-----LGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQT
 YARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATENLDE--FGIYGKSTFHPADGLSL
 DDKACAVG---LGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTL
 DDENFVMGGVTWRPTDATSLTFIFD--HL-DKDGVPGSGGHPLGTDFDRDQFFGEPDYYF
 FOLNVNNLFDEKHVASKDSGAVYYN-PG--RSILATLROSW 714
 SVWGTYTLEGDGARGDMLFGLGARYTDAYYTSITNTTSSESA--VVFDAAFTYKIQENTT
 NLWTTYQVTPELTIGG----GVNA-----MSGITSSAGMHAGGYATFDAMAAYRFTPKLK
 --PAAGS--DPTTGKQYEVGIK--YRPDAFPAMFTASVYDLTKGNITVFDQVTYLPQTVE
 SFGLRNDWLDLSETNLLAG---TRRAGNHREFTTRIGASYKVTEELAPYISYAESAAP--
 ----SANFYAPAPSIDWEDPIYSGGPGAMAPYASTNNDQQTNAIYLQQDLTFFDKLTV
 TDGSTVAGRYFFGNEKSTDQFVIDAHLVYEASLDNVESRTLFGADYNKYESD------
 SETNENSYSVLFD--HDFGNGLSFSSNARYSNLNDGFGSAYIGS-----TP
 NKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTA 348
 WDIN-----PDTVLGAGYLYQQRHLAPYNGLPADANNKL-PSLPQHVFVGAD---W
 FGEVYGTGGSFSHKELGFDFGDNLTADETL-----SYRLTGKFQRSDAEYDYSQ
 QGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAAD
 Proteobacteria; alpha subdivision;
 762
 (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence up)
(TrEMBLrel. 19, Last annotation)
 PRELIMINARY;
 ₽,
 83046 MW;
 10.9%;
 (Fragment).
 Score
 PRT;
 F489525A093B358E CRC64;
 410.5;
 762
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 Sphingomonadaceae;
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Length
762;
 682
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 403
 351
 307
 288
 241
 202
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QBXVB1
ID QBXVB1
ID QBXVB
AC QBXVB
DT 01-Mg
DT 01-Mg
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01-JUN-2002 (TrEMBLrel. 21, Last annotation
 Ralstonia solanacearum (Pa
Bacteria; Proteobacteria;
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RSC2920 OR RS00173.
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 ATFDAMAAYRFTPK-----LKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRY
 DLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVD
 WS-
 TLFDSFLRYDFANRFPRYKGLSLSINMRNIANKRYVATCTAASACYY-GQGRSLTLRLGY
 NGLAPYFSYAKSFQPQVSDPSTSLDGTPFKPTTGDQYEAGIRYQY-GKSIYITFGAYQIT
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 NTASQIGNYLPQAPKWMASLFIDQRIRHGFFTGLGIGGGVRYTGHSYGDTNNT-LSIPGY
 NSRDD-GIFL-LMPKHSANLWTTYQVT----PELTIGGGVNAMS----GITSSAGMHAGGY
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 DKNAAAPLNPNNKKTRYAALGKRVMEGV--ETEISGAVTPKWQIHAGYSYLHSQIK-TAS
 -----GKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLN
 GETVNRRAVEGRG----RSQGVATDTQLEGHVDTGAVRHVMLFGTDYFYTDWTHDRD----
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 DPFSLQQIEVLKGPSGALYGQTAPGGVVNLVTKRPTKKSQGEFFLQGAGY-THLGNWQGQ 215
 NLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGH---AAAGFGTHK---QYK 196
 FKRLRVTVGGRQDWAKDDTLNRLTGKR------YLTHSNAFTWRAGAVYLFD
 AD--DKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTL
 KWNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKT----PAGRPGCNT
 -----VLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKF
 AEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHET--FYAAAD--WDINPDT----
 ASGDVSEKLNKDGTLSGRI----VGLARYGDTQVNHVQTGRYYVSPSLTWEISPDTKWTV
 TIADALAYTAGVQAEPSGIDSRVDEVSVRGFGAGGFSSNNNFVDGLRLPSGGQWTR-TSF 156
 TFDQLARKTPGLRV-LSNDDGR-SSVYARGY---EYSEYN--IDG--LPAQMQSINGTLP
 EVKTAPSKKKDKSDVIVVTATG-LSQASSTTKTHTP--IIESPQSISIVSRDEIELRASP
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 629 IHORNVLTPDLDDPAGTHSTQTGEVRSQGFELEATVQPWAGWNVIAGYIYQDVRNTRAND 688
 617 SRDD--GIFLLMPKHSANLWTTYQVTPELTIGGGVNA-MSGITSSAG-----MHAGGYAT 668
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 474
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 EIEVQYĞSHVRKQVAGDFGGALDADĞKLSYRLTALARDĞNLPLGPFNDQRLMIAPSLTWK 325
 SHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACA 354
 243
 97 ROGDNTFTIEPAGSGABUTLPATVTTAAQAESANGPVHGYVARRSATGTKTDAPIEBİPÖ 156
 SVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVY--ARGYEYSEYNIDGLPAQ 133
 134 MOSINGTLPNL-----PAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQG 183
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 Gaps
 20
 VGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALN
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 ORQTQLGLYLQDQLKLGERWVFTLGGRHDWADTRTDDLLGGTTASQRDAAFTGRVGVYL
 LNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYK---GSYMDDRLNARVSFYR
 APYGISPYLSYSTSFNPTVGTDRNGQAFKPTKGRQVEAGVKVQAGS----RASVTASVFR
 MKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASN
 441 YG------RIDIDIQAQARFATGMVRHTLLAGVDYQR------QTT------
 ----GKTLHKASKTKFTGYAGAVYD
 Salamoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Salamoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Charlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Waissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).

EMBL: Al646072; CAD16627.1; -. Interpro; IPR000531; TonB_boxC.

Péan; PP00593; TonB_boxC; 1.
 ----QLPNTINLASWRVDPWQIECVELLRGPASVLYGQGDPGGTVNVTKQPTAEPIR
 184 HAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWD
 244 INPDTVLG--AGYLYQQRHLAPYNGLPA-----DANNKLPSLPQHVFVGA-DWNKFKMN
 10 INMTAATVLAALSS-----YNAIVTE
 Indels 190;
 DB 16; Length 801;
 Complete proteome.
SEQUENCE 801 AA; 87071 MW; 5577D637FF9203EA CRC64;
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MEDLINE=21681879; PubMed=11823852;
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443 NLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLND 502
 256 RVWGRKHMVYGIAEADAGDSSVLTLGGMYQKSREVPDFSGIILSCENQKTAPFSSTP--A 313
 NNKLPSLPQHVFVGADWNKFKWNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAG 331
 332 SKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRL----GNTANEFVI 387
 61 TVGTKIPASLREIPOSVSIITNOQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGY 120
 8 FRINWIAATVLAALSSS-----VFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAV 60
 Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=65699;
 748
 GAD----YNRERSTN-EQGRTTLYARGGLALNEFRSIP-OVDLIANARKGVRGYSHTVATE
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 VRKRPTKAFQGHAAAGFGTHK-QYKAEADVSGSLNSDGSVRGRVMAQTVGASP-RPAEKN
 ---NRHETFYAAADWDINPDTVLGAGYLYQQ------RHLAPYNGLPADA
 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAINE_2022556; PubMed=10761919;

Parkhill J., Achtuman M., James K.D., Bentley S.D., Churcher C., Rales S.R., Morelli G., Basham D., Brown D., Chillingworth T., Naeles S.R., Morelli G., Basham D., Erom D., Chillingworth T., Jagels K., Leather S., Moule S., Mungall K., Feltwell T., Hamlin N., Holroyd & Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Rutherford K.M., Simmonds M., Skelton J., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Montel B.G., Barrell B.G.; Barrell B.G.; Astrain of Neisseria meningitidis 22491.";
 22 FSLKILTVMLLSAYGSFADGVVPVSDGNTVSLDTVNVRGSHALSG-KTEKTRSYTIDRM
 121 EYSEYNIDGLPAQMQSING-----TLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNL
689 ASLDKWPIAIPTPRQIASLWTDYRIRSGVLQGVGIGAGVRYVSPTAGAPDNALRVPGYAL
 Ouery Match
Best Local Similarity 24.4%; Pred. No. 6.1e-16;
Matches 158; Conservative 111; Mismatches 258; Indels 121;
 FDAMAAYRFTPKLKLQINADNI FNRHYYARVGGANT FNI PGSERTWTANLRYSF
 Hypothetical protein, Complete proteome.
SEQUENCE 635 AA; 70757 MW; C477F457C36C41D2 CRC64;
 (TrEMBLrel. 15, Created) (TrEMBLrel. 15, Last sequence update) (TrEMBLrel. 19, Last annotation update)
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 Nature 404:502-506(2000).
EMBL; AL162756; CAB84891.1; -.
 Hypothetical protein NMA1663.
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| 음 성                                                                     | 용 성                                                                  | 유 상                                                  | 유 성                                                                  | 유                                                                 | 음 성                                                                 | 음 성                                                       | 3 m Q                                                                                                                                                              | RT RT RT RT RT RT RT RT RT RT RT RT RT R                                                                                                                                                                                                                                                                      | RA RA RA                                                                                                                                                                                                                                                                                                                                                                                                                         | 88888<br>88888                                                                                                                   |       | RES<br>P72<br>ID<br>AC                                         | 유 성                                                   | 유 성                                                        | 뮻                                        |
|-------------------------------------------------------------------------|----------------------------------------------------------------------|------------------------------------------------------|----------------------------------------------------------------------|-------------------------------------------------------------------|---------------------------------------------------------------------|-----------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------|-------|----------------------------------------------------------------|-------------------------------------------------------|------------------------------------------------------------|------------------------------------------|
| 331 GSKLGMKTÞAGRÞGCNTADDKACAVGLGTBIKQKALAFDASYSRÞFRLGNTANEFVIG 388<br>: | 271 ANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFA 330 | 229 KNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPAD 270 ; | 170 VNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVM-AQTVGASPRPAE 228 | 118 -RGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGI 169   : | 59 -AVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTDGLRVLSNDDGRSSVYA 117 | 9 RINMTA-ATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVT-EKNGDYSSF 58 | Query Match 10.6%; Score 402; DB 16; Length 863; Best Local Similarity 22.2%; Pred. No. 2e-15; Matches 171; Conservative 127; Mismatches 335; Indels 136; Gaps 31; | nce analysis of the genome of the unicellular cyanocystis sp. strain PCC6803. II. Sequence determinate genome and assignment of potential protein-coding s. 3:109-136(1996).  D90899; BAA16599.1; TO; IPRO0531; TonB_boxC. PP00593; TonB_boxC; 1.  te proteome.  CE 863 AA; 95026 MW; F8190445F9063CE4 CRC64; | [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=97061201; PubMed=8905231; KANNEKO T., Sato S., Kotani H., Tanaka A., Asamizu B., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S. | FHUA OR SLL1409.  Synechocystis sp. (strain PCC 6803).  Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  NCBI_TaxID=1148; | METT) | UULT 45<br>1599<br>P72599 PRELIMINARY; PRT; 863 AA.<br>P72599; | 552 VSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISGAV 594 : | 503 NNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNAR- 551 | 478ADKSEFVDKALAKBGIFNNAAQRFPNSLXDSSF 510 |

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 499 DLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMK 558
803 YTVGDYIIGNAAIFYQ-RDKYRVALNLRNFTNANYVRAVSGNQTGIEFG 850
 577 -RIGIYLQDQVSLLENLILVAGLRYDTITQNTNNLQTDFNQGGNTQQTDSAVTPRIGLLY 635
 528 IDYN----WSEESILTLEG-GPTSINVEDPDYNAIPKPN-----RSDLPLFGDTETSSN- 576
 389 ADYNRFRSTNEQGRTTLYARGGLALN----EFRSIPQVDLIANARKGVRGYSHTVATENL 444
 663 --AGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPG 709
 445 DEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKT-LHKASKTKFTGYA-----GAVY 498
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Search completed: December 18, 2002, 06:44:53 Job time : 62.0531 secs

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Copyright (c) 1993 - 2002 Compugen Ltd
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| ь             | 3776  | 100.0                    | 722   | 21 | AAB07697 | A Neisseria mening |
| N             | 3592  | 95.1                     | 691   | 21 | AAB07698 | A Neisseria mening |
| w             | 3244  | 85.9                     | 708   | 21 | AAY75566 | Neisseria meningit |
| 4.            | 821.5 | 21.8                     | 815   | 22 | AAU33610 | Pseudomonas aerugi |
| ហ             | 784   | 20.8                     | 725   | 20 | AAY38831 | Neisseria meningit |
| თ             | 784   | 20.8                     | 725   | 20 | AAY38834 | Neisseria gonorrho |
| 7             | 778   | 20.6                     | 725   | 20 | AAY38832 | Neisseria meningit |
| 00            | 765   | 20.3                     | 154   | 21 | AAY75565 | Neisseria gonorrhe |
| 9             | 737.5 | 19.5                     | 729   | 22 | AAU34539 | E. coli cellular p |
| 10            | 676.5 | 17.9                     | 623   | 20 | AAY38833 | Neisseria gonorrho |
|               |       |                          |       |    |          |                    |

New Neisseria meningitidis polypeptide useful for diagnosis of Neisseria infection and for development of vaccines against such infection -

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## ALIGNMENTS

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RESULT 1
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Neisseria meningitidis.
 WPI; 2000-476062/41.
N-PSDB; AAA59216.
 Ruelle J;
 WO200042193-A1.
 BASB053; Neisseria meningitidis infection; vaccine.
 A Neisseria meningitidis BASB053 polypeptide
 07-NOV-2000 (first entry)
 AAB07697;
 15-JAN-1999;
28-JAN-1999;
 10-JAN-2000; 2000WO-EP00137.
 20-JUL-2000.
 AAB07697 standard; Protein; 722 AA.
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 99GB-0000959.
99GB-0001903.
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standard; Protein; 691

AAB07698

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 The present sequence represents a Neisseria meningitidis BASB053 polypeptide. The BASB053 polypeptide, or an antibody immunospecific for BASB053 may be identified in a biological sample in order to diagnose a Neisseria meningitidis infection in an animal. The BASB053 polypeptides and polynucleotides may be used as vaccines, for generating an immune response in an animal. A composition comprising at least one antibody immunospecific for BASB053 may be used to treat humans infected with Neisseria meningitidis.
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 240
 120
 180
 300
 DWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFA 300
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 1 MGQFMSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAV 60
 181 FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAA
 1 MGQFMSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAV
 TVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTFGLRVLSNDDGRSSVYARGY
 EYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA
 FQCHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAA
 DWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFA
 DLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTE
 IKOKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIP
 QVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGK
 TLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYK
 TLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYK
 GSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQI
 GSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQI
 HAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAG
 601 HAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAG
 MHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRY
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 Length 722;
 Indels
 21;
 .;
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 æ
 100.0%; Score 3776;
100.0%; Pred. No. 0;
ive 0; Mismatches
 Page 55-56; 92pp; English
 722; Conservative
 Local Similarity
 722 AA;
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 Sequence
 Query Match
 SF
 SF
 Claim
 Matches
 61
 121
 241
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RESULT 2 AAB07698

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The present sequence represents a Neisseria meningitidis BASB053 polypeptide, or an antibody immunospecific for BASB053 may be identified in a biological sample in order to diagnose a Neisseria meningitidis infection in an animal. The BASB053 polypeptides and polynucleotides may be used as vaccines, for generating an immune response in an animal. A composition comprising at least one antibody immunospecific for BASB053 may be used to treat humans infected with Neisseria meningitidis.
 KTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANBFVIGADYNRFRS 396
 97 ARKTPGLRVLSNDDGRSSVYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGP 156
 Gaps
 HIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQL
 ARKTPGLRVLSNDDGRSSVYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGP
 SGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVM
 SGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVM
 AQTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLP
 AQTVGAS PRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLP
 SLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGM
 SLPQHVFVGADWNKFXMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGM
 HIKGORSYNAIVTEKNGDYSSFAVTVGTKIPASLREIPOSVSIITNOQVKDRNVDTFDQL
 ö
 aria meningitidis polypeptide useful for diagnosis infection and for development of vaccines against
 Length
 Indela
 BASB053; Neisseria meningitidis infection; vaccine.
 Query Match 95.1%; Score 3592; DB 21;
Best Local Similarity 99.7%; Pred. No. 3.8e-318;
Matches 684; Conservative 1; Mismatches 1;
 meningitidis BASB053 polypeptide
 (SMIK) SMITHKLINE BEECHAM BIOLOGICALS
 Claim 3; Page 56; 92pp; English
 99GB-0000959
 10-JAN-2000; 2000WO-EP00137
 99GB-0001903
 (first entry)
 Neisseria meningitidis
 WPI; 2000-476062/41.
 691 AA;
 N-PSDB; AAA59217
 WO200042193-A1.
 New Neisseria
 15-JAN-1999;
 28-JAN-1999;
 07-NOV-2000
 20-JUL-2000
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RESULT 3
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 01-MAY-1998;
31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
 09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
 Petersen
Tettelin
 Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septi antibacterial; gene therapy.
 AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, represent novel Neisseria meningitis and N.
 09-OCT-1998;
25-FEB-1999;
 30-APR-1999;
 WO9957280-A2
 Neisseria meningitidis
 Neisseria meningitidis ORF 760 protein sequence SEQ ID
 21-MAR-2000
 AAY75566
 Claim 2;
 Fraser C,
 11-NOV-1999.
 366
 999
 697
 909
 637
 546
 577
 486
 517
 426
 397
 457
 2000-062150/05.
DB; AAZ54328.
 ALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTT
 QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYA
 ARVGGANTFNI PGSERTWTANLRYSF
 YQVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYY
 ALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTT
 QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYA
 PADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTP
 PADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAYYDLNDNNSLYLSLSQLYTP
 TNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFH
 TNEQGRTTLYARGGLALNEFRS I PQVDL I ANARKGVRGYSHTVATENLDEFG I YGKSTFH
 Neisserial polypeptides nes and diagnostics -
 ARVGGANTFNI PGSERSLTANLRYSF
 YQVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYY
 CHIRON CORP.
INST GENOMIC RES.
 ټ. ر<u>ب</u>
 Page 1235; 1453pp; English.
 standard;
 Galeotti C,
 Pizza M,
Venter J
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 98US-0093758
98US-0094869
98US-0098994
98US-0099062
98US-0103794
98US-0103794
98US-0103794
98US-0103796
 99WO-US09346
 Protein;
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Rappuoli
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 Hickey
Ratti
 infection; meningitis; septicaemia;
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and AAY74253 to AAY75941 gonorrheae polynucleotides
 useful
 Masignani V,
Scalato E,
 antigens
 NO:2606
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Matches 627
 and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polypucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
 Sequence
 707
 721
 647
 661
 587
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 467
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 241
 241
 181
 181
 121
 121
 61
 61
 1 MGQFMSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAV 60
SF
 Ş
 HAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAG
 TLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYK
 QVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGK
 IKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIP
 DLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTE
 DWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFA
 FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAA
 EYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA 180
 TVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGY 120
 MGQFMSVFRINMTAATVLAALSSSVFAAQTEGLETVHIKGQRSYNAIATEKNGDYSSFAA 60
 DWDINPDTVLGAGYLYQQRRLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMHSHDVFA
 FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRRETFYAAA
 EYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA
 TVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGY
 THAGGYATFDAMAAYRFTPKLKLQINADNI FNRHYYARVGSESTFNI PGSERSLTANLRY
 TLHKASKTKFTSYAGAVYDIDGSNSLYASASQLYTPQTSIGTDGKLLKPREGNQFEIGYK
 YNGILQNARAGNKGFNHSVTEENLDETGLYAKTVFRPLEGLSLIAGGRVGHHKIESGDGK
 IKQKAFAVDASYSRPFALGNTANEFVIGADYNRLRSTNEQGRSTL--SKSVALDGFRALP
 DLKHYFGNGGYGKVGMRYSDRKADSNYTFAGSKLN------NTG--QADVAGLGTD
 627;
 708
 Similarity
 708
 Conservative
 ΑA;
 85.9%;
 33;
 Score 3244; DB 21;
Pred. No. 2.5e-286;
3; Mismatches 48;
 Length
 708;
 14;
 Gaps
 600
 180
 120
 720
 660
 586
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 540
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 420
 360
 300
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 240
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 406
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RESULT 4 AAU33610 4

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DGLPAQMQSI----NGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQG 183
 98GB-0019016.
97GB-0023516.
97GB-0024190.
97GB-0024386.
97GB-0025158.
 98WO-IB01665
 08-OCT-1999 (first entry)
 Neisseria meningitidis
 WO9924578-A2
 09-OCT-1998;
 18-NOV-1997;
27-NOV-1997;
10-DEC-1997;
 01-SEP-1998
 06-NOV-1997
 20-MAY-1999
 AAY38831;
 694
 220
 184
 244
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 360
 504
 477
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 RESULT 5
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 The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella premoitae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the antisense nucleic acids can also be used for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen compologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is also useful to screen compologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
 24;
 108 PQGNAITISVABAADSSV-----DLGATMITSNQL--GTITEDSGSYTPGTIATATRLV 159
 160 LTPRETPQSITVVTRQNMDDFGLNNIDDVMRHTPGITVSAYDTDRNNYYARGFSINNFQY 219
 Carr GJ;
 ASLREI PQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNI 127
 FRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIP 67
 Length 815;
 ö
 Trawick JD,
 polynucleotides for the identification and development
 antibiotics, comprise sequences of antisense nucleic acids
 Pseudomonas aeruginosa cellular proliferation protein #54.
 Conservative 145; Mismatches 312; Indels
 Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
 DB 22;
 Wall D,
 21.8%; Score 821.5; DB 29.0%; Pred. No. 2e-65;
 Example 3; Seg ID No 5106; 511pp; English
 ftp.wipo.int/pub/published_pct_sequences.
 Zyskind JW,
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AAU33610 standard; Protein; 815
 21-MAR-2000, 2000US-191078F.
23-MAY-2000; 2000US-206648F.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578F.
27-NOV-2000; 2000US-253625F.
22-DEC-2000; 2000US-253931P.
16-FEB-2001; 2001US-269308P.
 21-MAR-2001; 2001WO-US09180
 (first entry)
 Ohlsen KL,
Xu HH;
 (ELIT-) ELITRA PHARM INC
 Pseudomonas aeruginosa
 2001-611495/70.
 Similarity
 815 AA;
 N-PSDB; AAS51469
 WO200170955-A2.
 Haselbeck R,
Yamamoto RT,
 14-FEB-2002
 27-SEP-2001
 Matches 217;
 Seguence
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476
 645
 GEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTN--LDADGKLLKPRQGNQ 534
 GGGV------NAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNR 693
 Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
treatment; Neisseria infection; meningitis; septicaemia; gonorrhea.
||:|: ::: || || :: :|||||:| :|| DGIPSTARNVGYSAGNTLSDMAIYDRVEVLKGATGLLTGAGSLGATINLIRKKPTHEFKG
 HAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWD
 280 HVELGAGSWDNYRSELDVSGPLTESGNVRGRAVAAYODKHSFMDHYERKTSVYYGILEFD
 INPDIVLGAGYLYQQRHL--APYNG-LPA-DANNKLPSLPQHVFVGADWNKFKMNSHDVF
 ADLKHYPGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGT
 417 RSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIES
 FEVGYKGSYMDDRLNARVSFYRMKDKNAAAP----LINPNNKKTRYAALG-KRVMEGVET
 EISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQ---VTPELTI
 EIKQKALAFDASYSRPFRLGNTANEFVIG--ADYNRFRSTNEQGRTTLYARG-GLALNEF
 Neisseria meningitidis antigen encoded by ORF23.
 HYYARVGGANTFNI PGSERTWTANLRYSF 722
 788 TYYTNIGFYTSASY-GDPRNLMFSTRWDF 815
 AAY38831 standard; Protein; 725 AA.
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 organisms are
 and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORFS) AAZ11972-Z12358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria
 Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis and N. gonorrheeae antiqenic proteins. They are annoted by annotations
 Claim 4; Page 379-380;
 Proteins from Neisseria meningitidis and N. gono diagnosis, treatment and prevention of infection
 Grandi G,
 14-JAN-1998;
 infections, such as meningitis, septicaemia and gonorrhea. Bo organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
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 VYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR 174
 MTRFKYSLLFAALLPVYAQADVSVSDDPKPQESTELPTITVTADRT-----ASSNDGYTV 55
 1999-327407/27.
 RAADNLSLILGGRYTRYRTGSYDSRTQGMTYVSANRFTPYTGIVFDLTGNLSLYGSYSSL
 TAATDLIPGYWHADPRTHSASVSLIGKYRLFGREHDLIAGINGYKYAS-NKYGE-----
 RHRALNLFAGIEHRFN--
 KRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHE
 SGTHTPLGLPMTLREIPQSVSVITSQQMRDQNIKTLDRALLQATGTSRQIYGSDRAGYNY 115
 FAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQ-LARKTPGLRVLSNDD--GRSS
 MSVFRINMTAATVL-----AALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSS
 228;
 KTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSA 631
 YTPOTNLDADGKLLKPROGNQFEVGYKGSYMDDRLNARVSFYRMKDKN--AAAPLNPNNK 571
 HPADGLSLIGGGRLGHYKIESGEGKT--LHKASKTKFTGYAGAVYDLNDNNSLYLSLSQL 513
 GGLALNEFRSIPQVDLIANARKGVRGYSHTVA-----TENLDEFGI------YGKSTF
 ACAVGL---GTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYAR 408
 KMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDK 351
 ELYGILEYDIAPQTRVHAGMDYQQAKETADAPLSYAVYDSQGYATAFGPKDNPATNWANS
 TFYAAADWDINPDTVLGAGYLYQQRHL---APYNGLPADANNKLPSLPQHVFVGADWNKF 291
 KRLTRKPLFEVRAEAGNRKHFGLDADVSGSLNTEGTLRGRLVSTFGRGDSWRRRERSRDA 235
 LFARGSRIANYQINGIPVADALADTGNANTAAYERVEVVRGVAGLLDGTGEPSATVNLVR
NTYYRAANQAKTHGWEIEVGGRITPEWQIQAGYSQSKTRDQDGSRLNPDSV----PERSF
 FVPQSQKDEHGSYLKPVTGNNLEAGIKGEWLEGRLNASAAVYRARKNNLATAAGRDPSG-
 AAZ12259
 Masignani
 725 AA;
 Conservative
 RSI-----IPNAIPNAYEFSRTGAYPQPASFAQTIPQYGTRRQIGGYLATRF
 98GB-0000759
 ζ,
 20.8%;
 524pp; English.
 Pizza
 118;
 -----QDWKLKAEYDYTRSR--FRQPYGVAGVLSIDHN
 Score 784; DB 20;
Pred. No. 4.5e-62;
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06-NOV-1997;
14-NOV-1997;
 Amino acid sequences AAY38499-Y38944 represent Neisseria meningi and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORFs) AAZ11972-Z12358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria inferiors.
 Sequence
 infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
 Claim 4; Page 384; 524pp; English.
 diagnosis,
 Grandi G,
 Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine; treatment; Neisseria infection; meningitis; septicaemia; gonorrh
 P-PSDB; AAY38834.
 WPI; 1999-327407/27
 14-JAN-1998;
 27-NOV-1997
10-DEC-1997
 09-OCT-1998;
 WO9924578-A2
 Neisseria gonorrhoeae
 Neisseria gonorrhoeae antigenic protein encoded
 08-OCT-1999
 AAY38834;
 AAY38834 standard; Protein;
 20-MAY-1999
 (CHIR-)
 18-NOV-1997
 678
 672
 618
 632 NLWTTYQVTPEL----TIGGGV-----
26
 58
 Local
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 U
SGTHTPFGLPMTLREIPQSVSVITSQQMRDQNIKTLDRALLQATGTSRQIYGSDRAGYNY 115
 MAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIP-----GSERTWTANLRYSF 722
 FAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQ-LARKTPGLRVLSNDD--GRSS 114
 MSVFRINMTAATVL-----AALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSS 57
 MARYRFNPRAELSLNVDNLFNKHYRTQ-----
 KLFTAYHFAPEAPSGWTIGAGVRWQSETHTDPATLRIPNPAAKARAADNSRQKAYAVADI
 MTRFKYSLLFAALLPVYAQADVSVSDDPKPQESTELPTITVTADRT
 al Similarity
230; Conserv
 CHIRON SPA.
 from Neisseria meningitidis and N. s, treatment and prevention of infe
 Masignani
 725 AA;
 Conservative
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97GB-0023516.
 98GB-0000759
 97GB-0026147
 98WO-IB01665
 97GB-0025158
 97GB-0024386
 97GB-0024190
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 115;
 Pizza M,
 725
 Score 784; DB 20;
Pred. No. 4.5e-62;
5; Mismatches 321;
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 nd N. gonorrhoeae useful infection
 - PDRHSYGALRTVNAAFTYRF
 -NAMSGITSSAGMHAGGYATFDA 671
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 Length 725;
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 ORF23
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 gonorrhea.
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 SRNRALNIFAGIEHRFN------QDWKLKAEYDYTRSR--FRQPYGVAGVLSIDH 341
 STAATDLIPGYWHADPRTHSASMSLIGKYRLFGREHDLIAGINGYKYAS-NKYGERSIIP 400
 KRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQ-TVGASPRPAEKNNRH 233
 ETFYAAADWDINPDTVLGAGYLYQQRHL---APYNGLPADANNKLPSLPOHVFVGADWNK 290
 AELYGILEXDIAPQTRVHAGMDYQQAKETADAPLSYAVYDSQGYATAFGPKDNPATNWSN 294
 FKWNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADD 350
 KACAVGL---GTEIKOKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEOGRTTLYA 407
 454
 FHPADGLSLIGGGRLGHYKIESGEGKT--LHKASKTKFTGYAGAVYDLNDNNSLYLSLSQ 512
 LYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKN-AAAPLNPNNK 571
 NTYYRAANQAKTHGWEIEVGGRITPEWQIQAGYSQSKPRDQDGSRLNPDSV----PERSF 617
 632 NLWITYOVTPEL----TIGGGV------NAMSGITSSAGMHAGGYATFDA 671
VYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR 174
 KTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSA 631
 Neisseria meningitidis, Neisseria gonorrhoeae; antigen; vaccine;
treatment; Neisseria infection; meningitis; septicaemia; gonorrhea.
 | ||:
KHPTRKPLFEVRAEAGNRKHFGLGADVSGSLNAEGTLRGRLVSTFGRGDSWRQLER-SRD
 ------RSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKST
 KLFTAYHLAPEAPSGRTIGAGVRRQGETHTDPAALRIPNPAAKARAVANSRQKAYAVADI
 MAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIP----GSERTWTANLRYSF 722
 Neisseria meningitidis strain A antigen encoded by ORF23
 AAY38832 standard; Protein; 725 AA
 97GB-0023516.
97GB-0024190.
97GB-0024386.
97GB-0025158.
97GB-0026147.
 98WO-IB01665
 98GB-0019016
 (first entry)
 Neisseria meningitidis
 RGGLALNEF.
 WO9924578-A2
 27-NOV-1997;
10-DEC-1997;
14-JAN-1998;
 09-OCT-1998;
 08-OCT-1999
 20-MAY-1999
 06-NOV-1997
 14-NOV-1997
18-NOV-1997
 234
 351
 678
 116
 342
 408
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 175
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 RESULT 7
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Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORFs) AAZ11972-Z12358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
 ETFYAAADWDINPDTVLGAGYLYQQRHL---APYNGLPADANNKLPSLPQHVFVGADWNK 290
 | ::|| | | : || || || AELYGILEYDIAPQRATAFGPKDNPATNWAN 294
 SRHRALNLFAGIEHRFN------QDWKLKAEYDYTRSR--FRQPYGVAGVLSIDH 341
 342 NTAATDLIPGYWHADPRTHSASVSLIGKYRLFGREHDLIAGINGYKYAS-NKYGE---- 395
 512
 630
 ANLWITYQVTPEL----TIGGGV------NAMSGITSSAGMHAGGYATFD 670
 58 FAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQ-LARKTPGLRVLSNDD--GRSS 114
 VYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR 174
 KRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQ-TVGASPRPAEKNNRH 233
 351 KACAVGL---GTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYA 407
 Gaps
 for
 MSVFRINMTAATVL-----AALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSS
 SGTHTPLGLPMTLREIPQSVSVITSQQMRDQNIKALDRALLQATGTSRQIYGSDRAGYNY
 FKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADD
 FHPADGLSLIGGGRLGHYKIESGEGKT--LHKASKTKFTGYAGAVYDLNDNNSLYLSLSQ
 LYTPOTNLDADGKLLKPROGNOFEVGYKGSYMDDRLNARVSFYRMKDKN--AAAPLNPNN
 KKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHS
 RGGLALNEFRSI PQVDLIANARKGVRGYSHTVA-----TENLDEFGI-----YGKST
 Proteins from Neisseria meningitidis and N. gonorrhoeae useful diagnosis, treatment and prevention of infection
 Length 725;
 Scarlato V;
 Query Match 20.6%; Score 778; DB 20; Length 7. Best Local Similarity 29.7%; Pred. No. 1.6e-61; Matches 231; Conservative 117; Mismatches 317; Indels
 Rappuoli R,
 Σ
 Claim 4; Page 381; 524pp; English
 Pizza
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 Grandi G, Masignani
 1999-327407/27
CHIR-) CHIRON SPA
 725 AA;
 N-PSDB; AAZ12260
 Sequence
 26
 115
 116
 175
 176
 234
 235
 295
 408
 513
 571
 562
 291
 396
 455
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 Best Loc
Matches
 Query Match
 Fraser C, Ga.
Petersen J,
 AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrhaee polynucleotides and polypeptides. AAZ54576 and AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
 Sequence
 Claim 2;
 Novel Neisserial polypeptides predicted to be useful antigens vaccines and diagnostics -
 WPI; 2000-062150/05.
N-PSDB; AAZ54327.
 02-SEP-1998;
02-SEP-1998;
 01-MAY-1998;
 Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
 AAY75565 standard; Protein; 154
 09-OCT-1998;
 30-APR-1999;
 11-NOV-1999
 WO9957280-A2
 Neisseria gonorrheae.
 Neisseria
 21-MAR-2000
 AAY75565
 09-OCT-1998;
 617
 CHIR)
 671
 677
 Local Similarity
nes 143; Conser
 IMARYRFNPRAELSLNVDNLPNKHYRTQ------
 AMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIP-----GSERTWTANLRYSF 722
 CHIRON
 Page 1234; 1453pp; English.
 gonorrheae ORF 760
 Galeotti C, Grandi G, Pizza M, Rappuoli R,
 154
 Pizza M,
Venter J
 Conservative
 ON CORP.
GENOMIC RES.
 (first entry)
 98US-0103794.
98US-0103796.
99US-0121528.
 98US-0094869.
98US-0098994.
98US-0099062.
98US-0103749.
 B
 98US-0083758.
 99WO-US09346
 20.3%;
6,
 Score 765; DB 2:
Pred. No. 2e-61;
 protein
 Ä
 Mismatches
 Hickey E,
Ratti G,
 sequence
 DB 21; Length 154;
 -PDRHSYGALRTVNAAFTYRF 724
 SEQ
5
 Masignani V,
Scalato E,
 ID NO:2604.
 Indels
 Scarselli
 Mora M;
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 676
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Gaps

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RESULT 9
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The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The cC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in CC a wide variety of organisms. The present sequence represents an CC essential prokaryotic cellular proliferation protein.

CC of the printed specification, but was obtained in electronic
 WPI; 2001-611495/70.
N-PSDB; AAS52398.
 Example 3; Seq ID No 10132; 511pp; English.
 New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
 Haselbeck R,
Yamamoto RT,
 26-MAY-2000;
23-OCT-2000;
 21-MAR-2000;
23-MAY-2000;
 21-MAR-2001; 2001WO-US09180
 WO200170955-A2
 Escherichia coli
 Antisense; prokaryotic cellular proliferation antibiotic; antibacterial; drug design.
 E. coli cellular proliferation protein #120
 14-FEB-2002
 AAU34539;
 AAU34539
 16-FEB-2001;
 27-NOV-2000;
 569
 (ELIT-) ELITRA PHARM INC
 121
 689
 629
 61
 NNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPK
 NIFNRHYYARVGGTNTFNIPGSERSLTANLRYSF 154
 NIFNRHYYARVGGANTFNIPGSERTWTANLRYSF 722
 HSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINAD
 NNRNTRYAALGKRVMEGVETEISGAITPKWQIHAGYSYLHSQIKTAANPRDDGIFLLVPK
 HSANLWTTYQVTPGLTVGGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINAD
 standard;
 2000US-253625P.
2000US-257931P.
2001US-269308P.
 2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
 (first entry)
 Ohlsen
Xu HH;
 Protein;
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 Zyskind JW,
 729
 B
 Wall D,
 protein;
 Trawick JD,
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 Carr
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 688
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treatment; Neisseria infection; meningitis; septicaemia; gonorrhea
 97GB-0023516.
97GB-0024190.
97GB-0024386.
97GB-0025158.
97GB-0026147.
 98WO-IB01665
 .0019016
 Conservative
 >
 Neisseria gonorrhoeae
 Masignani
 Local Similarity
 WPI; 1999-327407/27.
 (CHIR-) CHIRON SPA.
 623 AA;
 P-PSDB; AAY38833.
 WO9924578-A2
 09-OCT-1998;
 06-NOV-1997;
14-NOV-1997;
18-NOV-1997;
 20-MAY-1999
 01-SEP-1998
 14-JAN-1998
 27-NOV-1997
10-DEC-1997
 Matches 198;
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 ---APLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYS-YLHSQIKTASNSRD 619
 STGTPIPGSNGETAYKAVDGTVSKGVEFELNGAITDNWQLTFGATRYI-----AEDNEG 620
 234
 TFYAA-ADWDINPDTVLGAGYLYQQRHL--APYNGLPA-DANNKLPSLPQHVFVGADWNK 290
 302
 362
 VIGADYNRFRSTNEOGRITLYARGGLALNEFRSIPOVDLIANARKGVRGYSHTVATENLD 445
 EIGSFYN-FNG-----WSPQSLAQDDTT 450
 504
 : :::: | | | | | | | | HWKSLYAATRVTLADPLHLILGARYTNWRVDT----LTYSMEKNHTTPYAGLVFDINDNW 506
 DGIFLLMPKHSANLWTTYQ--VTPELTIGGGVNAMSGITSSA------GMHAGGYATFD 670
 GFDYVGGTGWNSGKRKVDALDLFADGSYELFGRQHNLMFGGSYSKQNNRYFSSWANIFPD 422
 VGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYE 121
 Gaps
 QFMSVFRINMTAATV-LAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVT
 YSEYNIDGLPAQMQS----INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPT
 SREFKGDVSAEYGSWNKERYVADLQSPLTEDGKIRARI----VGGYQNNDSWLDRYNSEK
 -KAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGA---SPRPAEKNNRHE
 EF-GIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNN
 FKMNSHDVFADLKHYFGNGGYGKVCMRYSDRDADSNY----AFAGSKLGMKTP----
 ----AGRPGCNTADDKACAVGLGTE-----IKQKALAFDASYSRPFR--LGNTANEF--
 SLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAA-
 Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 105;
 671 AMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF 722
 Length
 Indels
 gonorrhoeae antigen encoded by partial ORF23
 22;
 Best Local Similarity 4/10, Mismatches 308; Matches 211; Conservative 148; Mismatches 308;
 19.5%; Score 737.5; DB 227.3%; Pred. No. 7.8e-58;
format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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 AAY38833 standard; Protein;
 (first entry)
 Local Similarity
 729 AA;
 08-OCT-1999
 Sequence
 Query Match
 AAY38833
 62
 122
 127
 187
 363
 423
 451
 179
 235
 303
 340
 507
 243
 446
 620
 505
 621
 564
 AAY38833
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meningitidis
 111 GRSSVYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIV 170
 NNRHETFYAAADWDINPDTVLGAGYLYQQRHL---APYNGLPADANNKLPSLPQHVFVGA 286
 TADDKACAVGL---GTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRT 403
 TLYARGGLALNEF------RSIPQVDLIANARKGVRGYSHTVATENLDEFGIY 450
 SIIPNAIPNAYEFSRTGAYPQPSSFAQTIPQYD----TRRQIGGYLAT----- 338
 GKSTFHPADGLSLIGGGRLGHYKIESGEGKT--LHKASKTKFTGYAGAVYDLNDNNSLYL 508
 ---RFRAADNLSLILGGRYSRYRAGSYNSRIOGMIYVSANRFIPYTGIVPDLIGNLSLYG 395
 10 GYNYLFARGSRIANYQINGIPVADALADIGNANTAAYERVEVVRGVAGLPDGTGEPSATV 69
 Proteins from Neisseria meningitidis and N. gonorrhoeae useful for diagnosis, treatment and prevention of infection
 NLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQ-TVGASPRPAEK
 -SRDAELYGILEYDIAPQTRVHAGMDYQQAKETADAPLSYAVYDSQGYATAFGPKDNPAT
 DWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCN
 : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 Amino acid sequences AAV38499-Y38944 represent Neisseria meningit and N. gonorrhoeae antigenic proteins. They are encoded by open treading frames (ORFs) AAZ11972-Z1358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
 95;
 623;
 17.9%; Score 676.5; DB 20; Length 30.0%; Pred. No. 2.2e-52; tive 90; Mismatches 277; Indels
 Scarlato
 ч,
Rappuoli
Pizza M,
 Claim 4; Page 383; 524pp; English.
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ARY5533
AAY7553
AAY7553
ID AAY75
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AC AAZ55
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 01-MAY-1998;
31-JUL-1998;
02-SEP-1998;
 Fraser C, G
Petersen J,
Tettelin H,
 09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
 antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
 AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54575 and AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the
 Neisseria meningitidis
 Neisseria meningitidis ORF 742 protein sequence SEQ ID NO:2540
 AAY75533
 Claim 2;
 Novel Neisserial polypeptides predicted vaccines and diagnostics -
 (CHIR)
 30-APR-1999;
 11-NOV-1999
 21-MAR-2000
 02-SEP-1998;
 572
 899
 512
 628
 456
 568
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 2000-062150/05.
DB; AAZ54295.
 VADIMARYRENERTELSLNVDNLFNKHYRTQ-----
 TFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIP----GSERTWTANLRYSF
 ERSFKLFTAYHLAPEAPSGRTIGAGVRRQGETHTDPAALRIPNPAAKARAVANSRQKAYA
 KHSANLWTTYQVTPEL----
 DQSGNTYYRAANQAKTHGWEIEVGGRITPEWQIQAGYSQSKPRDQDGSRLNPDSV----P
 SYSSLFVPQLQKDEHGSYLKPVTGNNLEADIKGEWLEGRLNASAAVYRARKNNLATAAGR 455
 PNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMP
 SLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKN-AAAPLN
 CHIRON CORP.
INST GENOMIC RES.
 e
 Page 1208; 1453pp; English.
 standard;
 Galeotti C, Grandi G,
Pizza M, Rappuoli R,
 Neisseria
 Pizza M,
Venter J
 (first
 98US-0094869.
98US-0098994.
98US-0099062.
98US-0103794.
98US-0103794.
98US-0103796.
99US-0121528.
 98US-0083758
 99WO-US09346
 Protein;
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 PDRHSYGALRTVNAAFTYRF
 Masignani
Scalato E,
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 NAMSGITSSAGMHAGGYA
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 , Mora M;
Scarselli
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 667
 567
 622
 722
 511
 627
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RESULT 12
AAY75534
ID AAY75
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AC AAY75
XX

AAY75534 standard;

Protein;

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AAY75534;

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 Matches 170;
 Query Match
Best Local :
 be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
 Sequence
 310
 237
770
 707
 710
 651
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 603
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 493
 472
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 412
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 352
 396
 292
 386
 232
 368
 181
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 w
 NTYLGEDWGRLSADKYNLFSGFKHVFDNGWQLNAEVSYTKNESDAKVGQFFLKNEYAAGL
 HVFVGADWNKFKMNSHDVFADLKHYFGNG--------------
 GYSYLHSQIKTAS------NSRDD--GIFLLMPKHSANLWTTYQV-TPELTIGGGVN
 FALFYLEQKNRTVVDFGYVPGAGGKQGSFQTVAKPIGKVVSRGAEFELSGELNEDWKVFA
 VSFYRMKDKN-----AAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHA
 ADGLSLIGGGRLGHYKIESGEGKTL----KFTG
 VR-----VATENLDEFGIYGK---
 WQAYDEKGNRTVYAEECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKG
 --STNEQGRTTLYARGGLALNEFRSIPQ-----
 FVGYAYGDEKIRSEYLEIYERRYRVRPNTGATHGVYAGSCQEEPDGDLSSPLVRGHKEPD
 SRRAAERKAGFDKCMSDPFALDFICQGSWGDPGVDA--DKA-----EFVDKALAKEGI
 SGEDAVGFLTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR 180
 -GYGKVGM-----
 YGIAEADAGDSSVLTLGGMYQKSREVPDFSGIILPCENQKTAPFSSTP--ACNRPLQLPR
 YAAADWDINPDTVLGAGYLYQQ-------RHLAPYNGLPADANNKLPSLPQ
 IPGSERTWIANLRYSF 722
 AQSGTSSLYNIRQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFY
 AMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY----YARVGGANTFN
 GYTYNKSRYKNAAEVNAERLAKNSSADPYNFSNFTPVHI FRFGTSFHI PNTGLTVGGGVS
 YAGITYDLTPQQSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLQGRLNAS
 YAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGK-LLKPRQGNQFEVGYKGSYMDDRLNAR
 TGRLHLLGG--LHYTRYETSQTKDMPVRYGQPASDFQTASSIRADQDHYTAKMQGHKLTP
 NKIQETNPDGTPAFTGFSGTVPVWKTVKVADDHVPALYNYAKYLNTNKTHSLTASTRFNV
 FNNAAQRFPNSLYDSSFNRKATANRRYSYMPLRHTKDDRQWGIKLDLTGTYGLFGREHDF
 -----PFR-----
GEPRTVSMKLDWQF
 Similarity
 783 AA;
 Conservative
 AGSKLGMKTPA-----
 10.6%;
 ----SNYAF----
 ; 68
 Score 400.5; DB 2
Pred. No. 4.6e-27;
 Mismatches 212;
 GRPGCNTADDKACAVGLGTEIKQKALA----
 -----VDLIANARKG
 21;
 Indels
 Length
 -----STFHP
 LGNTANEF
 325;
 Gaps
 649
 551
 492
 457
 431
 385
 231
 367
 329
 309
 60
 280
 706
 709
 650
 602
 589
 411
 351
 395
 291
 769
 529
 28;
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---FDASYSR------PFR----
 AAB68923 standard; Protein; 702 AA.
 Neisseria meningitidis protein #22
 TTLYARGGLALNEFRSIPQ-----
 99EP-0401764.
 (first entry)
 Neisseria meningitidis.
 GRLGHYKI ESGEGKTL-
 Nassif X, · Tinsley C;
 WPI; 2001-082916/10
 783
 716 ANLRYSF 722
 rni5; rth; tolC.
 Meningococcus;
 777 MKLDWQF
 EP1069133-A1
 13-JUL-1999;
 13-JUL-1999;
 18-APR-2001
 17-JAN-2001
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 27;
 AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N gonorrheae polynucleotides and polypeptides. AAZ54575 to AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseriab bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
 Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
 Ξ
 237 YAAADWDINPDTVLGAGYLYQQ-------RHLAPYNGLPADANNKLPSLPQ 280
 ---DSNYAFA--G 331
 SDEDAVGFLTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR 180
 SKLGMKTPAGRPGCNTAD---DKACAVGLG-----TEIKQKALA------ 367
 Mora M;
Scarselli
 281 HVFVGADWNKFKMNSHDVFADLKHYFGNG-------GYGKVGMRY-----
 Novel Neisserial polypeptides predicted to be useful antigens for
 Neisseria meningitidis ORF 742 protein sequence SEQ ID NO:2542
 Mismatches 220; Indels 307;
 DB 21; Length 783;
 Masignani V,
Scalato E, S
 10.5%; Score 397.5; DB 2
21.3%; Pred. No. 8.6e-27;
ive 92; Mismatches 220
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 Hickey F
Ratti (
 Claim 2; Page 1209; 1453pp; English.
 Grandi G,
Rappuoli R,
 98US-0083758.
98US-0094869.
98US-0099062.
98US-0103749.
98US-0103794.
 99WO-US09346
 99US-0121528
(first entry)
 Matches 168; Conservative
 (CHIR) CHIRON CORP. (GENO-) INST GENOMIC RES.
 vaccines and diagnostics
 Galeotti C,
, Pizza M,
 Venter JC;
 Neisseria meningitidis
 2000-062150/05.
 Similarity
 783 AA;
 N-PSDB; AAZ54296.
 WO9957280-A2
 30-APR-1999;
 Petersen J,
Tettelin H,
 11-NOV-11999
 09-OCT-1998
 02-SEP-1998
 02-SEP-1998
 25-FEB-1999
 SDRDA-
 Fraser C,
 Sequence
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KIRSEYLEIYERRHRVRPNTGATHGVYAGSCOGEPDGDLSSPLVRGHKEPDWQAYDEKGN 360
 433
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| :: | | :: | | :
| RTVYABECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNPD 420
 GTPAFTGFSGTVPVWKTVKVADDHVPALYNYAKYLNTNKTHSLTAGTRFNVTGRLHLLGG 480
 501
 DNNSLYLSLSQLYTPQTNLDADGK-LLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDK 560
 KTAS------NSRDD--GIFLLMPKHSANLWTTYQV-TPELTIGGGVNAMSGITSSA 659
 719 NIROGGYGLIDGFVRYELGKHAKLSLIGTNINGRIYFENNYNRIRGANNFY--GEPRIVS 776
 -----LGNTANEFVIGADY--N
 -----VDLIANARKGVR-----
 -----HKASKT---KFTGYAGAVYDLN
 --LHYTRYETSQTKDMPVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLT
 |:| | :::: | |:| | :| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:
 N-----AAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQI
 660 GMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY----YARVGGANTFNIPGSERTWT
 meningitis; bacteraemia; vaccine; dsbA; fhaB; fhuA;
 -----GYSHT-----VATENLDEFGIYGK------STFHPADGLSLIGG
 (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
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Matches 171;
 The present invention provides the protein and coding sequences of several genes from Nelsseria meningitidis. These include the dsbA, fhaB, fhuB, rnts, rth17, rth18, rth19, rth20, rth21 and tolC genes. These can be used in the diagnosis and treatment of infection by the bacterium, which can lead to meningitis and bacteraemia, and in vaccines to prevent
 Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
 Claim 3; Fig 22B; 240pp;
 N-PSDB;
 660
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 569
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 462
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 345
 277
 286
 233
 173
 178
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 œ
 SLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA-----GAVYDLNDNNSLYLSLSQLYTP
 ITVKLDN-----GLKWT------GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
 LGWNH-KNVNVTFAAANLLNQKYW---
 CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
 NFKQSRNIGAVYGSWANRSINMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPS
 VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG 119
 FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA
 infection.
 AAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF
 MPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG-----
 KNNPYIYAVSGKHRSRGVELSAIGQIIPK-KLYLRGSLGVMQAKVVEDKENPDRVGIHLN
 NNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD---
 YGGRGYLSIDTSSAAVFNAAÞEYTRQYETGVKSSWLDDRLSTTLSAYQIERFNIRYRPDP
 ----QTNLDADGKLL----KPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNP
 KFVLGGRYDKYTFNSENKLT---GNSRQYSGHSFSPNIGAVWNINPVHTLYASYNKGFAP
 LGYRGSF-----TVP-INPYDRASWPASGRLQPILTQNRHKADSYGIFVQNIFSATPDL
 LYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADGL
 QQT-----DNKTLSSNLTLNGDYTIGRFENHLTVGMDYSR----EHRNPT
 AHRNDFYKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW
 ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG
 PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG
 TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGASPR
 FQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSKYA
 YEYSEYNI---DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
 VTRNGQL---IKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFLRG
 FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
 Similarity
 AAF56463
 702
 Conservative
 A
 9.9%;
 136;
 English.
 Score 375.5; DB 2
Pred. No. 7.3e-25;
 Mismatches 336;
---RSDSMPGNPRGYTARVNYRF
 -GVIGT
 GKRYGYNSRNKEVTTLPGFARVDAM
 DB 22; Length
 Indels
 722
 GYATFDAM
 127;
 702;
 GIFLL 625
 Gaps
 prevent
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 172
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 672
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 404
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ARBESULT 14
ARB68921
ID ARB68
XX ARB68
XX ARB68
XX Neiss
XX Menir
XX Menir
XX Menir
XX III-JI
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 Query Match
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Matches 175
 The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, f feveral genes from Neisseria meningitidis. These to to genes. These fhuA, rni5, rth17, rth18, rth19, rth21 and tolC genes. These be used in the diagnosis and treatment of infection by the bacterium which can lead to meningitis and bacteraemia, and in vaccines to pre
 Sequence
 Immunogenic polypeptides derived from Neisseria meningitidis nucleic acids that encode them, useful for diagnosing and vacagainst Neisseria infections e.g. bacteremia and meningitis -
 WPI; 2001-082916/10.
N-PSDB; AAF56461.
 AAB68921 standard;
 Claim 3; Fig 20B; 240pp; English
 13-JUL-1999;
 13-JUL-1999;
 17-JAN-2001.
 EP1069133-A1
 Neisseria meningitidis
 AAB68921;
 Nassif
 rni5;
 Meningococcus;
 18-APR-2001
 (INRM) INSI
(PLAC) MAX
 284
 230
 224
 170
 176
 114
 118
 61
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 8
VGADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGR
 infection.
 YANFKOSRNIGAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVS
 RPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGAS
 RGFQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSK 169
 RGYEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRK 175
 FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA
 FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
 PSITVKLDN-----GLKWT-----
 PRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVF
 VTRNGQL---IKETPQTIDTL---NIKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFL
 VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFD--QLARKTPGLRVLSNDDGRSSVYA 117
 al Similarity 22.5%; Pr
175; Conservative 134;
 rth;
 ×
 INSERM INST NAT SANTE & RECH MEDICALE MAX PLANCK GES FOERDERUNG WISSENSCHAFT
 meningitidis protein
 Tinsley
 tolc
 702
 (first
 A
 meningitis;
 99EP-0401764
 99EP-0401764
 Ç
 Protein;
 22.5%;
 entry)
 bacteraemia; vaccine;
 702
 Score 374.5; DB Pred. No. 9e-25;
 Mismatches
 A
 -GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMG
 WISSENSCHAFTEN
 BB
 326;
 22;
 dsbA;
 Indels
 Length
 fhaB;
 143;
 bacterium,
 and
 fhuA;
 Gaps
 prevent
 283
 229
 60
 59
 274
 223
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us-09-889-267-2.rag

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The invention relates to a library of DNA fragments of Escherichia colistrains comprisaing polymucleotides (ABABS17-3 and ABAB8813) and encoded proteins (ABBS2459-ABBS2919 and ABBS2954-ABBS2094) of nature B2/D+A-. The polymucleotides have potential antiinflammatory,
 ō
 PGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGR 402
 AWQQT------DNKTLSSNFTLNGDYTIGRFENHLTVGMDYSR----EHRN 374
 -- QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDK 560
 485 APYGGRGGYLSIDTLSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYQIERP 539
 NAAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD 620
 664
F-AHRNDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNY 333
 meningitis;
 Escherichia coli strains for the given strain comprises polynucleotides
 TTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPAD
 GLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA-----GAVYDLNDNNSLYLSLSQLY
 ---GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG------
 GYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF
 antibacterial;
 ပ်
 Bscherichia coll; B2/D+A-; antiinflammatory; antibacterial;
immunosuppressive; extra-intestinal infection; phylogeny; n
systemic infection; non-diarrhoeal infection; septicaemia;
 Tinsley
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 (INRM) INSERM INST NAT SANTE & RECH MEDICALE
 Nassif
 Escherichia coli polypeptide SEQ ID NO 263.
 pyelonephritis; antibiotic resistance
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 Clermont
 Example 6; Fig 6; 646pp; English.
 663
 A library of DNA fragments of phylogenic determination of a
 ABB52462 standard; Protein;
 12-MAR-2001; 2001WO-EP03445
 2000FR-0003145
 2001FR-0001449
 (first entry)
 ŝ
 Bonacorsi
 WPI; 2001-550253/61.
 nature B2/D+ A- -
 Escherichia coli
 TP-----
 WO200166572-A2
 10-MAR-2000;
 02-FEB-2001;
 11-FEB-2002
 13-SEP-2001
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 Bingen
 334
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275
 375
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32;
 compositions used to treat, palliate or prevent extra-intestinal E. colinfections. The polypeptides are useful for determining the phylogenic group of a given E. coli strain. These polypeptides can detect and treat an undesired development of E. coli, particularly an extra-intestinal infection that include systemic and non-diarrhoeal infections such as septicaemia, pyelonephritis and meningitis this is particularly advantageous as bacterial resistance is increasing with the more frequent use of broad spectrum antibiotics.
antibacterial and immunosuppressive activity as part of pharmaceutical
 407
 ATSSSFGGGT------GQLDITGPIEGTQLAYRLTGEVQDEDYWRNFGKERSTFI 235
 322
 567
 672
 610
 A-AADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSH 296
 381
 ALSSSVFAA------QTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASL
 71 REIPOSVSIITNOQVKDRNVDTFDQLARKTPGLRVLSNDDG--RSSVYARGYEYSEYNID
 72 LDIPQVVNTVSDQVLENQNATTLDEALYNVSNV-VQTNTLGGTQDAFVRRGF---GANRD
 GLPAQMQSINGTLPNLF--AFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAA
 G-SIMTNGLRTVLPRSFNAATERVEVLKGPASTLYGILDPGGLINVVTKRPEKTFHGSVS
 297 DVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVG
 -----RVTAYDATTGTLTRRVDATQGSTQRMHATRADL-----QGNVDIAGFYNE
 -RGGLALNEFRSIPQVDLIA-----FGIY
 323 LLGGVSY-EYYDLLRTDMIRCKKAKDFNIYNPVYGNTSKCTTVSASDSDQTIKQENYSAY
 GKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTK---FTGYAGAVYDLNDNNSLY
 AQDALYLTDNWIAVAGIRYQYYTQYAGKGRPPNVNTDSRDEQWTPKLGLVYKLTPSVSLF
 LSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLN
 442 ANYSQTFMPQSSIASYIGDLPPESSNAYEVGAKFELFDG-ITADIALFDIHKRNVLYTES
 DGIFLLMPKHSANLWTTYQV-----TPELTIGGGVNAMS--GITSSAGMHAGGYATFDAM
 A----GFGTHKOYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEK----NNRHETFY
 568 PNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQI-----KTASNSRD
 APSLTWFGDNATVTMAEY----HL----------NSQWT-----
 357 LGTEIKQKALAFDASYSRPFR----LGNTANEFVIGADYNRFRSTNEQGRTTLYA---
 Indels 198;
 AAYRFTPKLK----LOINADNIFNRHYY-ARVGGANTFNIPGSERTWTANLRYSF
 Length 663;
 285;
 9.8%; Score 371; DB 22;
llarity 22.1%; Pred. No. 1.7e-24;
Conservative 121; Mismatches 285;
 Similarity
 663 AA;
 Matches 171;
 Sequence
 Query Match
 Local
 673
 20
 129
 128
 187
 187
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 620
 278
 451
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AAB68926 standard; Protein; 703

RESULT 16 AAB68926 ID AAB689

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 Query Match
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Matches 174
 The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, fhab, thab, rnis, rth17, rth18, rth19, rth21 and tolC genes. These can be used in the diagnosis and treatment of infection by the bacterium, which can lead to meningitis and bacteraemia, and in vaccines to prevent
 Sequence
 Claim 3; Fig 25B; 240pp; English.
 Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
 N-PSDB;
 WPI; 2001-082916/10.
 (INRM)
 EP1069133-A1
 Neisseria meningitidis.
 Meningococcus; meningitis; bacteraemia; vaccine; dsbA; fhaB; fhuA;
 Neisseria meningitidis protein #25
 13-JUL-1999;
 13-JUL-1999;
 17-JAN-2001
 18-APR-2001
 AAB68926;
 337
 173
 345
 286
 233
 226
 117
 120
 61
 60
 Local Similarity
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 œ
 NFKQSRNIGAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPS
 CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
 FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
 infection.
 AHRNDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW
 ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG
 ITVKLDN-----GLKWT------GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
 PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG
 TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGASPR
 FQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSKYA
 YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP, 177
 VTRNGQL---IKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFLRG
 VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG
 FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA
 rth;
 ×
 AAF56466.
 INSERM INST NAT SANTE & RECH MEDICALE.
MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 703
 tolC.
 Tinsley
 Conservative
 (first entry)
 B
 99EP-0401764.
 99EP-0401764
 Q
 9.8%;
 DNKTLSSNFTLNGDYTIGRFENHLTVGMDYSR----
 131;
 Score 371; DB 22;
Pred. No. 1.9e-24;
 Mismatches
 Length 703;
 Indels
 140;
 -EHRNPT
 Gaps
 prevent
 404
 225
 172
 119
 59
377
 336
 344
 232
 116
 60
 276
 33;
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AAY75568
ID AAY75
XX AAY75
XX Neiss
XX Neiss
XX Neiss
XX Neiss
XX Neiss
XX Neiss
XX Neiss
XX Neiss
XX Neiss
XX AAY7
DR AAY7
PR 31-JU
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 09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
 01-MAY-1998;
31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
 antigenic; diagnosis; immunc antibacterial; gene therapy.
 Novel Neisserial polypeptides predicted vaccines and diagnostics
 N-PSDB; AAZ54330
 (CHIR)
 30-APR-1999;
 11-NOV-1999
 Neisseria meningitidis
 Neisseria meningitidis; Neisseria
 Neisseria meningitidis ORF 761
 21-MAR-2000
 AAY75568
 WPI; 2000-062150/05
 Fraser C,
 rettelin
 Petersen
 654
 601
 621
 542
 562
 487
 516
 430
 461
 378
 405
 LSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA-----GAVYDLNDNNSLYLSLSQLYT
 FARVDAMLGWNH-KNVNITFAAANLLNQKYW-----RSDAMPGAPRTYTARVNYSF
 YATEDAMAAYRETPKLKLQINADNI FNRHYYARVGGANTENI PGSERTWTANLRYSE
 RVGIHLNNTSNVTGNLFFRY--TPTENLYGEI----GVTGT-GKRYGYNSRNKEVTTLPG
 LGYSRAFTA-----SIDPYDRASWPASGRLQPILTQNRHKADSYGIFVQNIFSATPD
 L-YARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADG
 AAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD-
 PYGGRGGYLSINTSSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYQIERFN
 LKFVLGGRYDKYTFNSENKLT---GSSRQYSGHSFSPNIGAVWNINPVHTLYASYNKGFA
 IRYRPDEQNDPYTWAVGGKHRSRGVELSAIGQIIPK-KLYLRGSLGVMQAKVVEDKENPD
 -GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG------G
 INST
 CHIRON CORP
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 standard;
 Galeotti C,
 Venter JC;
 GENOMIC
 (first entry)
 Pizza M,
 98US-0103749.
98US-0103794.
98US-0103796.
 98US-0083758
98US-0094869
 99US-0121528
 98US-0099062
 98US-0098994
 99WO-US09346
 Protein;
 -QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKN
 RES.
 immunogenic;
 Grandi G,
Rappuoli R,
 703
 protein sequence
 B
 gonorrheae;
 Hickey E,
Ratti G,
 infection;
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 useful
 Masignani V, Mora M;
Scalato E, Scarselli
 antigen; vaccine;
meningitis; septicaemia;
 SEQ ID NO:2610
 antigens
 for
 703
 722
 665
 600
 620
 561
 486
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AAZ53015 to AAZ54536,

AAZ54577 to AAZ54615,

and

AAY74253

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AAY75941

Claim 2;

Page 1238; 1453pp;

English.

```
represent novel Neisseria meningitis and N. gonorrheae polymucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polymucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polymucleotides of the invention may also be used in gene therapy protocols.
 33;
 :: : | |::|:| |: EQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSKYA 172
 225
 285
 233 ITVKLDN-----GLKWT------GYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF- 276
 377
 430
 516
 999
 602 VGIHLNNTSNVTGNLFFRY--TPTENLYGEI----GVTGT-GKRYGYDSRNKEVTTLPGF 654
 VIVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG 119
 VTRNGQL---IKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFLRG 116
 YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
 ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG 344
 404
 461
 487
 --- QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA 562
 Gaps
 FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA 59
 PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG
 AHRNDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW
 178 TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR------VMAQTVGASPR
 QQT------DNKTLSSNLTLNGDYTIGRFENHLTVGMDYSR----EHRNPT
 LYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADGL
 SLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA----GAVYDLNDNNSLYLSLSQLYTP
 KFVLGGRYDKYTFNSENKLT---GSSRQYSGHSFSPNIGAVWNINPVHTLYASYNKGFAP
 YGGRGGYLSIDTLSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYQIERFNI
 563 AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD--
 CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
 Y9------
 ATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF 722
 138;
 Length 703;
 Indels
 -GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG-
 llarity 22.4%; Pred. No. 2.3e-24;
Conservative 130; Mismatches 334;
 DB 21;
 9.8%; Score 370; DB 21; 22.4%; Pred. No. 2.3e-24;
 Best Local Similarity
Matches 174; Conserv
 703 AA;
 Sequence
 Query Match
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The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, fhaB, fhuA, rniS, rthl7, rth18, rth19, rth20, rth21 and tolC genes. These can be used in the diagnosis and treatment of infection by the bacterium, which can lead to meningitis and bacteraemia, and in vaccines to prevent
 nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
 120 YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
 178 TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGASPR 225
 PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG 28S
 Gapa
 meningitis; bacteraemia; vaccine; dsbA; fhaB; fhuA;
 FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
 PHLALLPTLIIA--SPPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA
 VTVGTKI PASLREI PQSVSI I TNQQVKDRNVDTFDQLARKT PGLRVLSNDDGRSSVYARG
 233 ITVKLDN-----GLKWT-----GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
 ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLCMKTPAGRPG
 Length 703,
 9.8%; Score 370; DB 22; Length 7. ilarity 22.4%; Pred. No. 2.3e-24; Conservative 130; Mismatches 334; Indels
 (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 $
 Neisseria meningitidis protein #15
 English
 AAB68916 standard; Protein; 703
 99EP-0401764.
 99EP-0401764
 Claim 3; Fig 15B; 240pp;
 Neisseria meningitidis.
 Nassif X, Tinsley C;
 WPI; 2001-082916/10.
N-PSDB; AAF56456.
 Best Local Similarity
Matches 174; Conserv
 703 AA;
 rnis, rth, told
 such infection.
 Meningococcus;
 13-JUL-1999;
 EP1069133-A1
 13-JUL-1999;
 18-APR-2001
 17-JAN-2001
 Sequence
 AAB68916
 Query Match
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RESULT 19
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 Fraser C, - Thersen J, F
 Novel Neisserial polypeptides predicted vaccines and diagnostics -
 09-OCT-1998;
 02-SEP-1998;
 01-MAY-1998;
31-JUL-1998;
 30-APR-1999;
 WO9957280-A2
 Neisseria meningitidis
 antigenic; diagnosis; immuno antibacterial; gene therapy.
 Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
 Neisseria
 21-MAR-2000
 AAY75567 standard; Protein;
 09-OCT-1998;
 02-SEP-1998
 11-NOV-1999
 (GENO-)
 (CHIR)
 431
 655
 621
 543
 563
 488
 517
 462
 378
 337
 345
 405
 2000-062150/05
DB; AAZ54329.
 ATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF
 KFVLGGRYDKYTFNSENKLT---GSSRQYSGHSFSPNIGAVWNINPVHTLYASYNKGFAP
 SLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA-----GAVYDLNDNNSLYLSLSQLYTP
 õ
 ARVDAMLGWNH-KNVNVTFAAANLFNQKYW-----RSDSMPGNPRGYTARVNYRF
 RYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPK-KLYLRGSLGVMQAKVVEDKENPDR
 AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD--
 YGGRGGYLSIDTLSSAVFNAD-----PEYTROYETGVKSSWLDDRLSTTLSAYQIERFNI
 L----GFSSAFSASINPYD---RASWPASGRLQPILTQNRHKADSYGIFVQNIFSATPDL
 LYARGGLALNEFRS I POVDLI ANARKGVRGYSHTVATEN---LDEFGI YGKSTFHPADGL
 CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
 VGIHLNNTSNVTGNLFFRY--TPTENLYGEI----GVTGT-GKRYGYDSRNKEVTTLPGF
 -GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG------
 CHIRON CORP.
 INST
 -----QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA
 meningitidis ORF
 Galeotti C,
 GENOMIC RES.
 Venter
 (first entry)
 Pizza M,
 98US-
 98US-0103796
99US-0121528
 98US-0103749
 98US-0099062
 98US-0098994
 98US-0083758
98US-0094869
 99WO-US09346
 ----DNKTLSSNLTLNGDYTIGRFENHLTVGMDYSR-----EHRNPT
 -0103794
 Grandi G,
Rappuoli R,
 761 protein sequence SEQ
 703
 B
 Hickey E,
Ratti G,
 to be useful antigens
 Masignani V,
Scalato E, (
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 NO:2608
 Scarselli
 Mora
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 666
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 Query Match
Best Local S
Matches 174
 AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polymucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polymucleotides of the invention may also be used in gene therapy protocols.
 Sequence
 Claim 2;
655
 667
 602
 543
 563
 488
 517
 431
 462
 405
 337
 345
 277
 286
 233
 226
 173
 178
 117
 120
 61
 60
 Local Similarity
 8
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 VGIHLNNTSNVTGNLFFRY--TPTENLYGEI----GVTGT-GKRYGYNSRNKEVTTLPGF
 AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD--
 KFVLGGRYDKYTFNSENKLT---GSSROYSGHSFSPNIGAVWNINPVHTLYASYNKGFAP
 SLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA-----GAVYDLNDNNSLYLSLSQLYTP
 LYARGGLALNEFRS I POVDLIANARKGVRGYSHTVATEN --- LDEFGIYGKSTFHPADGL
 CNTADDKACAVGLGTEIKOKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEOGRTT
 ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG
 ITVKLDN-----GLKWT------GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
 PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG
 FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
ARVDAMLGWNH-KNVNVTFAAANLLNQKYW-----RSDSMPGNPRGYTARVNYRF
 ATFDAMAAYRFTEKLKLQINADNI FNRHYYARVGGANTFNI PGSERTWTANLRYSF
 RYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPK-KLYLRGSLGVMQAKVVEDKENPDR
 YGGRGGYLSIDTLSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYQIERFNI
 L----GFSSAFSASINPYD---RASWPASGRLQPILTQNRHKADSYGIFVQNIFSATPDL
 QQT-----DNKTLSSNLTLNGDYTIGRFENHLTVGMDYSR----EHRNPT
 FQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSKYA 172
 YEYSEYNI---DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP
 VTRNGQL---IKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFLRG
 VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG
 FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA
 AHRNDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW
 -GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG
 Page 1237; 1453pp;
 703 AA;
 Conservative
 -QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA
 9.7%;
 130;
 English
 Score 368; DB 21;
Pred. No. 3.5e-24;
 Mismatches
 Length
 Indels 138;
 703;
703
 Gaps
 666
 601
 461
 404
 177
 119
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 59
 654
 620
 542
 562
 487
 516
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 377
 336
 344
 276
 285
 232
 225
 33
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rni5;
277
 345
 337
 405
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 462
 431
 517
 488
 667
 655
 621
 RESULT 21
 AAB68920
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 33;
 The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, fhaB, fhuA, rniS, rthl7 rthl8, rth19, rth20, rth21 and tolC genes. These can be used in the diagnosis and treatment of infection by the bacterium, which can lead to meningitis and bacteraemia, and in vaccines to prevent
 Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
 VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG 119
 120 YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
 178 TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR------VMAQTVGASPR 225
 PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG 285
 286 ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG 344
 Gaps
 FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA 59
 meningitis; bacteraemia; vaccine; dsbA; fhaB; fhuA;
 NFKQSRNIGAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPS
 ITVKLDN-----GLKWT------GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
 Mismatches 334; Indels 138;
 Length 703;
 (INRM) INSERM INST NAT SANTE & RECH MEDICALE. (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
 9.7%; Score 368; DB 22; 22.4%; Pred. No. 3.5e-24;
 ż
 Neisseria meningitidis protein #26
 Claim 3; Fig 26B; 240pp; English.
 AAB68927 standard; Protein; 703
 Conservative 130;
 99EP-0401764
 99EP-0401764
 (first entry)
 Neisseria meningitidis
 Nassif X, Tinsley C;
 WPI; 2001-082916/10.
N-PSDB; AAF56467.
 Query Match
Best Local Similarity
 703 AA;
 rth; told
 Meningococcus;
 such infection
 EP1069133-A1
 13-JUL-1999;
 13-JUL-1999;
 18-APR-2001
 17-JAN-2001
 Matches 174;
 Sequence
 rni5;
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The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the debh, fhab, fhuh, rni5, rth17, rth18, rth19, rth20, rth21 and tolc genes. These can be used in the diagnosis and treatment of infection by the bacterium,
 Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
| |- |- | : | | : | | : | ARRIDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW 336
 -----QTNLDADGKLLKPRQGNQFBVGYKGSYMDDRLNARVSFYRMKDKNA 562
 563 AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD-- 620
 999
 CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
 ---DNKTLSSNLTLNGDYTIGRFENHLTVGMDYSR----EHRNPT
 LYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADGL
 SLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA-----GAVYDLNDNNSLYLSLSQLYTP
 YGGRGGYLSIDTLSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYQIERFNI
 -GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG------GY
 602 VGIHLNNTSNVTGNLFFRY--TPTENLYGEI----GVTGT-GKRYGYNSRNKEVTTLPGF
 fhaB; fhuA;
 ARVDAMLGWNH-KNVNVTFAAANLLNOKYW-----RSDSMPGNPRGYTARVNYRF
 ATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF
 Meningococcus; meningitis; bacteraemia; vaccine; dsbA;
 T SANTE & RECH MEDICALE. FOERDERUNG WISSENSCHAFTEN.
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 Neisseria meningitidis protein #19.
 Claim 3; Fig 19B; 240pp; English.
 standard; Protein; 702
 99EP-0401764.
 99EP-0401764
 (first entry
 (INRM) INSERM INST NAT
(PLAC) MAX PLANCK GES F
 Neisseria meningitidis.
 Nassif X, Tinsley C;
 2001-082916/10.
 OQT----
 N-PSDB; AAF56460
 rth; told.
 13-JUL-1999;
 13-JUL-1999;
 EP1069133-A1
 18-APR-2001
 17-JAN-2001.
 AAB68920
 AAB68920;
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RESULT 22
AAB18720
ID AAB1
XX
AC AAB1
XX
DT 22-J
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DE A Ne
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BASB
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 Query Match
 Matches 176;
BASB082; BASB083; BASB091; BASB092; BASB0101; infection; vaccine;
 A Neisseria meningitidis BASB083 polypeptide
 AAB18720
 AAB18720 standard;
 Sequence
 such
 22-JAN-2001
 651
 620
 560
 514
 375
 403
 334
 343
 275
 284
 230
 170
 176
 114
 118
 665
 484
 427
 459
 224
 61
 60
 Local
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 AWQQT-----DNKTLSSNFTLNGDYTIGRFENHLTVGMDYSR----EHRN
 KNAAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRD
 RGYEYSEYNI--DGLFAQMQSINGTLFNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRK 175
 n can lead infection.
 PGFARVDAMLGWNH-KNVNITFAAANLLNQKYW-----RSDAMPGAPRTYTARVNYSF
 D---GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG------
 FAPYGGRGGYLSINTSSSAVFNAD----PEYTROYETGVKSSWLDDRLSTTLSAYQIER
 DGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA----GAVYDLNDNNSLYLSLSQL
 PTLGYSRAFTA-----SIDPYDRASWPASGRLQPILTQNRHKADSYGIFVQNIFSAT
 TTL-YARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPA 458
 F-AHRNDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNY
 VGADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGR
 PRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVF
 YANFKOSRNIGAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVS
 RPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGAS
 RGFQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSK
 VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFD--QLARKTPGLRVLSNDDGRSSVYA 117
 FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
 -GYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF 722
 PDRVGIHLNNTSNVTGNLFFRY--TPTENLYGEI----GVTGT-GKRYGYNSRNKEVTTL
 FNIRYRPDEQNDPYTWAVGGKHRSRGVELSAIGQIIPK-KLYLRGSLGVMQAKVVEDKEN
 PDLKFVLGGRYDKYTFNSENKLT---GSSRQYSGHSFSPNIGAVWNINPVHTLYASYNKG
 PGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGR
 PSITVKLDN-----GLKWT------GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMG
 VTRNGQL---IKETPQTIDTL---NIKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFL
 FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA 60
 Similarity
 lead to meningitis and bacteraemia, and in vaccines to prevent
 702 AA
 Conservative 131;
 (first
 Protein;
 entry)
 9.7%;
 -QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKD
 703
 Score 367.5; DB : Pred. No. 3.9e-24
 Mismatches 327;
 B
 DB 22;
 Indels
 Length
 145;
 702;
 Gaps
 342
 597
 559
 426
 374
 402
 333
 223
 169
 59
 664
 619
 538
 483
 513
 274
 229
 35;
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gene therapy; upper respiratory tract infection; bacteremia; meningitis;
invasive bacterial disease.
Neisseria meningitidis
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PXRXRXRX 21-SEP-2000

07-MAR-2000; 12-MAR-1999; 2000WO-EP01955 99GB-0005815 99GB-0009094

21-APR-1999; 23-APR-1999; 28-APR-1999; 07-MAY-1999; 99GB-0009503. 99GB-0009787. 99GB-0010710

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS

Defrenne Ç Delmelle Ç Ruelle J;

N-PSDB; AAA75745. 2000-602119/57

Novel polypeptides designated BASB 082, 083, 091, 092, and 101 derived from meningococcus bacterium useful for producing vaccines against infections and in diagnostic assays -

Claim 3; Page 102-104; 108pp; English.

The present sequence represents a BASB083 polypeptide. The specification describes BASB082, BASB083, BASB091, BASB092, and BASB0101 polypeptides. The polynucleotides and polypeptides sequence and for diagnostic reagents and for diagnosing N. meningitidis infection. The polynucleotides may be used as hybridisation probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding BASB082, BASB083, BASB091, BASB092 or BASB101 polypeptides and to isolate cDNA and genomic clones of other genes that have a high identity particularly high sequence identity to BASB082, BASB083, BASB091, BASB092 or BASB101 genes. The vaccine compositions are useful for inducing an immunological response in humans. The polynucleotides encoding BASB082, BASB093, BASB091, BASB092 or BASB101 polypeptides are useful in gene therapy to induce an immunological response. The polypeptides are useful for treating upper respiratory tract infection, invasive bacterial diseases, such as bacteremia and meningitis. such as

Sequence 703 AA;

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 Matches
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Best Local Similarity
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 178
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 YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
 FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
 ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG
 ITVKLDN-----GLKWT------GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
 PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG
 NFKQSRNIGAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPS
 TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGASPR 225
 FQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSKYA
 VTRNGQL---IKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFLRG
 VTVGTKIPASLREIPOSVSIITNOQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG
 FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA
 Conservative 133;
 9.7%; Score 366; DB 21; 22.2%; Pred. No. 5.4e-24; tive 133; Mismatches 333;
 Length
 Indels 138;
 Gaps
 116
 119
 60
 59
 344
 276
 285
 232
 33
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to prevent

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which can lead to meningitis and bacteraemia, and in vaccines
 Similarity
 702 AA;
 such infection.
 18-APR-2001
 Matches 177;
 Sequence
 Query Match
 AAB68919
 117
 178
 226
 345
 9
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 405
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 429
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 The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, fhab, thi5, rthl7, rthl8, rth19, rth20, rth21 and tol6 genes. These can be used in the diagnosis and treatment of infection by the bacterium,
 L----GFRRNFTASIDPYD---RASRPASGRLQRILAQDRHKADSYGIFVQNIFSATPDL 430
 516
 Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
| | | : || : || : | AHRNDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW 336
 377
 461
 487
 562
 563 AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD-- 620
 RYRPDEQNDPYTWAVGGKHRSRGVELSAIGQIIPK-KLYLRGSLGVMQAKVVEDKKNPDR 601
 -GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG-------GY 666
 602 VGIHLNNTSNVTGNLFFRY--TPTENLYGEI----GVTGT-GKRYGYNSRNKEVTTLPGF 654
 CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT 404
 fhuA;
 | | : : : : | | : | | -----DNKTLSSNFTLNGDYTIGRFENHLTVGMDYSR-----EHRNPT
 ------QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA
 SLIGGGRLGHYKI ESGEGKTLHKASKTKFTGYA----GAVYDLNDNNSLYLSLSQLYTP
 488 YGGRGGYLSINTSSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYQIERFNI
 LYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADGL
 ATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF 722
 meningitis; bacteraemia; vaccine; dsbA; fhaB;
 (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
 Ź
 Neisseria meningitidis protein #21
 Claim 3; Fig 21B; 240pp; English.
 AAB68922 standard; Protein; 702
 99EP-0401764
 99EP-0401764
 (first entry)
 Neisseria meningitidis
 Tinsley C;
 2001-082916/10.
 N-PSDB; AAF56462
 rth; tolC.
 Meningococcus;
 337 QOT----
 EP1069133-A1
 13-JUL-1999;
 13-JUL-1999;
 18-APR-2001
 17-JAN-2001
 Nassif X,
 AAB68922;
 rni5;
 277
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 RESULT 23
 AAB68922
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VIVGTKIPASLREIPOSVSIITNOOVKDRNVDTFDOLARKTPGLRVLSNDDGRSSVYARG 119
 YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVWRGPSGLFDSSGEMGGIVNLVRKRP 177
 :: :| ||: ||: | |: ERVEILKGPSSVLYGRTNGGGVINMVSKYA 172
 173 NFKQSRNIGAVYGWANR-SLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPS 231
 PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG 285
 286 ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG 344
 | | | : ||: ||: | | AHRNDFVKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW 335
 CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT 404
 L-YARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADG 460
 LGYNRAFSA----SINPYD---RASWPASGRLQPILTQNRHKADSYGIFVQNIFSATPD 428
 LSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA----GAVYDLNDNNSLYLSLSQLYT 515
 --GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG------G, 665
 600 RVGIHLNNTSNVTGNLFFRY--TPTENLYGEI----GVTGT-GKRYGYDSRNKEVTTLPG 652
 FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA 59
 702
 Meningococcus; meningitis; bacteraemia; vaccine; dsbA; fhaB; fhuA;
 TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGASPR
 ITVKLDN-----GLKWT-----GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
 336 QQT------DNKTLSSNFTLNGDYTIGRFENHLTVGMDYSR----EHRNPT
 P-----QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKN
 486 PYGGRGGYLSIDTLSSAVFNAD-----PEYTROYETGVKSSWLDDRLSTTLSAYOIERFN
 562 AAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD-
 Indels 141;
 : | | | | : | : | | | : | | EARVDAMLGWNH-KNVNTFAAANLFNQKYW-----RSDSMPGNPRGYTARVNYRF
 666 YATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF
Length 702;
 DB 22;
 9.7%; Score 364.5; DB 22;
llarity 22.8%; Pred. No. 7.3e-24;
Conservative 129; Mismatches 330;
 ż
 Neisseria meningitidis protein #18
 AAB68919 standard; Protein; 703
9.7%;
 (first entry)
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rni5; rth; tolC

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 Query Match
Best Local
 Matches
 Sequence
 Claim 3; Fig 18B; 240pp; English.
 Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
 N-PSDB;
 Nassif X,
 (INRM)
 13-JUL-1999;
 13-JUL-1999;
 17-JAN-2001
 EP1069133-A1
 Neisseria meningitidis
 thuA,
 several
 345
 277
 286
 233
 173
 117
 462
 226
 120
 61
 9
 we present invention provides the protein and coding sequences of wveral genes from Neisseria meningitidis. These include the dsbA, fhaB, war all genes from Neisseria meningitidis. These include the cabA, fhaB, war, rni5, rth17, rth18, rth12, rth21 and tolC genes. These can war, used in the diagnosis and treatment of infection by the bacterium, the cabacterium and the diagnosis and bacteraemia, and in vaccines to prevent ich can lead to meningitis and bacteraemia, and in vaccines to prevent
 ហ
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 2001-082916/10.
 CNTADDKACAVGLGTEIKOKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
 infection.
 SLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA-----GAVYDLNDNNSLYLSLSQLYTP
 LYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADGL
 ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG
 ITVKLDN-----GLKWT------GOYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
 NFKQSRNIGAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPS
 FQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSKYA 172
 FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA
 FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA 59
 L----GFSSAFSASINPYD---RASWPASGRLQPILTQNRHKADAYGIFVQNIFSATPDL
 AHRNDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW
 PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG
 TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGASPR
 YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
 VTRNGQL---IKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFLRG
 VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG
 Similarity
 AAF56459.
 INSERM INST NAT SANTE & RECH MEDICALE MAX PLANCK GES FOERDERUNG WISSENSCHAFT
 Tinsley
 703 AA;
 Conservative
 99EP-0401764.
 99EP-0401764
 ----DNKTLSSNLTLNGDYTIGRFENHLTVGMDYSR----EHRNPT
 Ç
 9.6%;
 FOERDERUNG WISSENSCHAFTEN
 130;
 Score 363; DB 2
Pred. No. 1e-23;
 Mismatches
 ::
::
 DB 22;
334;
 Length 703;
 Indels
 138;
 Gaps
 461
 404
 336
 232
 225
 116
 119
 60
 516
 377
 344
 33;
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RESULT 25
AAB68917
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 PT XXX PAXX PAXX PT XXX PT XXX
 X S X
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 XZ
 Query Match
Best Local S
Matches 142
 The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, fhab, fhub, rni5, rth17, rth18, rth19, rth20, rth21 and tolC genes. These can be used in the diagnosis and treatment of infection by the bacterium, which can lead to meningitis and bacteraemia, and in vaccines to prevent
 Sequence
 Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
 such infection.
 Claim 3; Fig 16B; 240pp; English.
 WPI; 2001-082916/10.
N-PSDB; AAF56457.
 Nassif X,
 13-JUL-1999;
 13-JUL-1999;
 17-JAN-2001.
 EP1069133-A1
 Neisseria meningitidis
 Meningococcus; meningitis; bacteraemia; vaccine; dsbA;
 Neisseria meningitidis protein
 18-APR-2001
 AAB68917
 (INRM)
 655
 602
 621
 543
 563
 488
 431
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 œ
 AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD--
 KFVLGGRYDKYTFNSENKLT---GSSRQYSGHSFSPN1GAVWN1NPVHTLYASYNKGFAP
FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA
 FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
 ARVDAMLGWNH-KNVNITFAAANLLNQKYW----
 ATEDAMAAYRETPKLKLQINADNIFNRHYYARVGGANTENIPGSERTWTANLRYSF 722
 VGIHLNNTSNVTGNLFFRY--TPTENLYGEI----GVTGT-GKRYGYNSRNKEVTTLPGF
 -GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG-----
 RYRPDEQNDPYTWAVGGKHRSRGVELSAIGQIIPK-KLYLRGSLGVMQAKVVEDKENPDR
 YGGRGGYLSINTSSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYQIERFNI 542
 rth;
 INSERM INST NAT SANTE & RECH MEDICALE MAX PLANCK GES FOERDERUNG WISSENSCHAFT
 Similarity
 standard; Protein;
 Tinsley
 tolc
 697 AA;
 Conservative
 (first entry)
 99EP-0401764.
 99EP-0401764.
 -QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA 562
 8.4%;
 FOERDERUNG WISSENSCHAFTEN
 107;
 697
 Score 316.5; DB 2
Pred. No. 1.7e-19;
7; Mismatches 286
 B
 -RSDAMPGAPRTYTARVNYSF
 DB 22;
 Length
 fhaB;
 697
 107;
 fhuA;
 703
 ģ
 Gaps
 prevent
 60
 666
 109
 620
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 225
 378 L---GFSSAFSASINPYD---RASWPASGRLQPILTQNRHKADSYGIFVQNIFSATPDL 430
 516
 YGGRGGYLSIDTLSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYQIERFNI 542
 YEYSEYNI - - DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
 PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG 285
 ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG 344
 AHRNDFVKDKLOVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW 336
 404
 OOT------DNKTLSSNLTLNGDYTIGRFENHLTVGMDYSR-----EHRNPT 377
 461
 ------QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA 562
 \mathsf{the}
VTVGTKI PASLREI PQSVSI I TNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG
 TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGASPR
 fhuy;
 ITVKLDN-----GLKWT-----GOYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
 CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
 LYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDBFGIYGKSTFHPADGL
 SLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA----GAVYDLNDNNSLYLSLSQLYTP
 Immunogenic polypeptides derived from Neisseria meningitidis and
 meningitis; bacteraemia; vaccine; dsbA; fhaB;
 AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGY 604
 (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
 Æ
 Neisseria meningitidis protein #24
 697
 AAB68925 standard; Protein;
 99EP-0401764
 99EP-0401764
 (first entry)
 Neisseria meningitidis
 Tinsley C;
 2001-082916/10.
 rnis; rth; tolC.
 Meningococcus;
 EP1069133-A1
 13-JUL-1999;
 13-JUL-1999;
 17-JAN-2001.
 18-APR-2001
 Nassif X,
 AAB68925;
 N-PSDB;
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 178
 488
 345
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 117
 226
 286
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The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dabA, fhaB, fhuA, rni5, rth17, rth18, rth19, rth20, rth21 and tolC genes. These can be used in the diagnoals and treatment of infection by the bacterium, which can lead to meningitis and bacteraemia, and in vaccines to prevent such infection.
acids that encode them, useful for diagnosing and vaccinating Neisseria infections e.g. bacteremia and meningitis -
 YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
 PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG 285
 344
 | | | : :||::| AHRNDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW 336
 404
 337 QQT------DNKTLSSNLTLNGDYTIGRFENHLTVGMDYSR-----EHRNPT 377
 461
 430
 516
 487
 -- QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA 562
 542
 Gaps
 59
 9
 FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
 VTVGTKI PASLREI PQSVSII TNQQVKDRNVDTFDQLARKT PGLRVLSNDDGRSSVYARG
 :: :| || : : | : : | || : : | || EQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSKYA
 TKAFQCHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGASPR
 233 ITVKLDN-----GLKWT-----GQÝTÝDNVERTÞDRSPTKSVYDRF-GLÞYRMGF-
 ADWINKFKWINSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG
 LYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADGL
 L----GFSSAFSASINPYD---RASWPASGRLQPILTQNRHKADSYGIFVQNIFSATPDL
 462 SLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA-----GAVYDLNDNNSLYLSLSQLYTP
 KFVLGGRYDKYTFNSENKLT---GSSRQYSGHSFSPNIGAVWNINPVHTLYASYNKGFAP
 CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
 Indels 107;
 Length
 AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGY 604
 DB 22;
 8.4%; Score 316.5; DB 22;
llarity 22.1%; Pred. No. 1.7e-19;
Conservative 107; Mismatches 286;
 543 RYRPDPKNNPYIYAVSCKHRSRGVELSAIGQIIPKKTLSARF
 Escherichia coli polypeptide SEQ ID NO 1209.
 Ź
 Claim 3; Fig 24B; 240pp; English
 721
 standard; Protein;
 (first entry)
 Local Similarity
 697 AA
 11-FEB-2002
 Matches 142;
 nucleic a
against N
 Sequence
 ABB52899
 Query Match
 ABB52899
 178
 00
 9
 120
 111
 226
 277
 345
 563
 286
 405
 378
 517
 ABB52899
 RESULT
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Query Match
Best Local Sim
Matches 171;
 B2/D+A- The polynucleotides have potential antiinflammatory, antibacterial and immunosuppressive activity as part of pharmaceutical compositions used to treat, palliate or prevent extra-intestinal E. coli infections. The polypeptides are useful for determining the phylogenic group of a given E. coli strain. These polypeptides can detect and treat an undesired development of E. coli, particularly an extra-intestinal infection that include systemic and non-diarrhoeal infections such as septicaemia, pyelonephritis and meningitis this is particularly advantageous as bacterial resistance is increasing with the more
 Sequence
 The invention relates to a library of DNA fragments of Escherichia colistrains comprising polynucleotides (ABA88577-ABA88729 and ABA89533) and encoded proteins (ABB52459-ABB52919 and ABB52954-ABB53094) of natural
 A library of DNA fragments of phylogenic determination of a
 10-MAR-2000; 2000FR-0003145
02-FEB-2001; 2001FR-0001449
 Escherichia coli; B2/D+A-; antiinflammatory; antibacterial; immunosuppressive; extra-intestinal infection; phylogeny; meningitis; systemic infection; non-diarrhoeal infection; septicaemia;
 Example 6; Fig
 WPI; 2001-550253/61
 13-SEP-2001
 Escherichia coli.
 pyelonephritis; antibiotic resistance.
 12-MAR-2001; 2001WO-EP03445
 (INRM) INSERM INST NAT SANTE &
 331
 284
 227
 231
 167
 171
 119
 122
 61
 65
 N
 9
 NRHETFYAAADWDINPDTVL---GAGYLY-QQRHLAPYNGLPADANNKLPSLP----QHV 282
 NLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKN
 LGTKSWIETPYSSTTVTKEMIENQQAQSVSEMLKYSPSTQMQARGGMDVGRPQ--SRGMQ 118
 RINMTAATVLAALSSSV----FAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGT 64
GSKLGMKTPAG--RPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIG
 ALSTAGN--DLTTDTISTRLIHYFNDDWSMNAG---VGWQQADRAMRSVSSKILNNQGDI
 FVGADWNKFKMNSHDVFADLKHYFG----NGGYGKVGMRYSDRDADS-----
 LRRKLVSVALDWNIQPGTQLQLDASHYEFIQKGYVGSFNYGP---NVKLPSAPNPKDKNL
 NFVAKRPTEETLRKVTLGYQSRSAFTGHADLGGHFDENKRFGYRVNLLDQEGEGNVDDST
 GSVVANSRLDGLNIVSTTAFPVEM---
 YS---EYNIDGL------PAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIV 170
 KIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSN---DDGRSSVYARGYE 121
 KTOITFAALLPALASFIPLHAHASSTSEDEMI-VTGNTAADTTDSAAGAGFKTNDIDVGP 60
 M
 B2/D+ A-
 Similarity
 use of broad spectrum antibiotics.
 Bonacorsi
 721 AA;
 Conservative
 6; 646pp;
 8.3%;
 ß
 English
 Clermont 0,
 127;
 Score 313.5; DB 2
Pred. No. 3.4e-19;
 Escherichia coli
given strain comp
 RECH
 Mismatches
 ----LERMDVLNSLTGALYGPASPAGQF
 MEDICALE.
 Nassif X,
 comprises polynucleotides
 344;
 22;
 Tinsley
 Indels 119;
 Length 721;
 ç
 NYAFA
 Gaps
 230
 166
388
 338
 330
 283
 226
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Sequence

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be used in the diagnosis and which can lead to meningitis

The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, fh fhub, rni5, rth17, rth18, rth19, rth20, rth21 and tolC genes. These c be used in the diagnosis and treatment of infection by the bacterium,

and bacteraemia, and

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vaccines

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RESULT 28
AAB68918
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 Immunogenic polypeptides derived from Neisseria meningitidis and nucleic acids that encode them, useful for diagnosing and vaccina against Neisseria infections e.g. bacteremia and meningitis -
 Claim 3;
 N-PSDB;
 Nassif X,
 17-JAN-2001.
 Neisseria meningitidis protein
 AAB68918;
 AAB68918 standard;
 13-JUL-1999;
 13-JUL-1999;
 EP1069133-A1
 Neisseria meningitidis
 Meningococcus;
 18-APR-2001
 (INRM) INSERM INST
 rni5;
 339
 662
 675
 607
 622
 550
 563
 494
 509
 436
 449
 392
 389
 2001-082916/10
 TRYTTKVSNVPTTFRVVVNNVFDKHYWASIFPSGTDGDNGS
 IFLLMPKHSANLWTTYQV--TPELTIGGGVN----AMSGITSSAGMHAGGYATFDAMAA
 FAYLDTDNV---YKEQGNQVNNGLELTAAGNVWQGLNIYSGVTFLDPKLKDTANASTSNK
 SYADSLEOGGTAPTDESVKNAGQTLNPYRSKQYEVGLKSDI--GEMNLGAALFRL--ERP
 SRSMKDSTAAGRERVLSNTA-----GLNGHIDTGSIGHDLSLSTTGYVWSLYSAKGTG
 YRFTPKLK-----LQINADNIFNRHYYARVGGANTFNIPGS 710
 QVVGVPKVQANLLAEYSLPSIPEWVYSANVHYTGKRAANDTNTS---YASSYTTWD--LG
 AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIK-TASNSRDDG
 --DTVTFTPQWSAMFYLSQSWLQTKNYDKHGNQTNQVDENGLSPNAALMYKITPNTMAYV
 IYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYL
 SSYS-----WGTTNMYHPD--AIDE----QGD--GKIRTGGPRYRSSVNTQQSVTLG
 ADYNR FRSTNEQGRTTLYARGGLALNE FRS I PQVDLI ANARKGVRGYSHTVATENLDE FG
 rth;
 AAF56458.
 INSERM INST NAT SANTE & RECH MEDICALE
 Fig 17B;
 SLSQLYTPQT--NLDADGKLLKPRQGNQFEYGYKGSYMDDRLNARVSFYRMKDKNA
 tolc
 Tinsley
 (first
 99EP-0401764
 99EP-0401764
 meningitis; bacteraemia; vaccine; dsbA; fhaB;
 240pp; English.
 ç,
 GES
 Protein;
 entry
 FOERDERUNG
 700
 #17.
 B
 WISSENSCHAFTEN
 702
 vaccinating
 fhuA;
 the
 606
 508
 448
 661
 674
 621
 549
 562
 493
 435
 391
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24;
 61 VTRNGQL---IKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFLRG 116
 :: : | | |:: | | |: EQADASDIYRDGVRESGQ-VRRSTANI ---ERVEILKGPSSVLYGRTNGGGVINMVSKYA 172
 VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG 119
 YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
 TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR------WMAQTVGASPR 225
 PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG 285
 233 ITVKLDN-----GLKWT-----GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF- 276
 ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG 344
 404
 L-YARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADG 460
 LSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA-----GAVYDLNDNNSLYLSLSQLYT 515
 P-----QTNLDADGKLL---KPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPL 566
 Gaps
 5 FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA 60
 "deduced residue from nucleotide sequence
is His, this differs from Seq ID5, residue
is Gly"
 -----LETVHIKGQRSYNAIVTEKNGDYSSFA
 345 CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
 QQT------DNKTLSSNFTLNGDYTIGRFENHLTVGMDYSR----EHRNPT
 66
 adhesin; plasmid pear; vector; vaccine; intestine colonisation.
 Length 700;
Query Match

8.1%; Score 307.5; DB 22; Length
Best Local Similarity 21.9%; Pred. No. 1.1e-18;
Matches 138; Conservative 109; Mismatches 285; Indels
 NPNNKKTRYAALGKRVMEGVETEISGAVTPK 597
 DAENNPYTWAVGGKHRSRGVELSAIGQIIPK 577
 Location/Qualifiers
 æ
 FRINMTAATVLAALSSSVFAAQTAD-
 AAR75366 standard; Protein;
 entry)
 (first
 Escherichia coli
 Misc-difference
 WO9600233-A1
 13-MAY-1996
 04-JAN-1996.
 AAR75366;
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 120
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 173
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 RESULT 29
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98 ILIDGVRQGGSSDVTPNGFSAMNTGFMPLAAIERIEVIRGPMSTLYGSDAMGGVVNIIT 157
 YNIDGL------PAQMQSIN-GTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR 174
 158 RKNADKWLSSVNAGLNLQESNKWGNSSÖFNFWSSGPLVDDSVSLOVRGSTOOROGSSVTS 217
 -----TRORYDNRDGG----LGSLT 273
 GMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRF 394
 -TENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASK 487
 SLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLS--NDDGRSSVYARGY--EYSE 124
 MAQTVGAS-PRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNK 274
 488 TKFTGYAGAVYDLNDNNSL-----YLS--LSQLYTPQTNLDADGKL-----LKPRQ 531
 A candidate adhesin (AAR75366) was identified that is a homologue of the IrgA protein of Vibrio cholerae. The adhesin enables Escherichia coli O157:H7, an antibiotic-resistant, virulent and common food-borne pathogen, to adhere to epithalial cells. Recombinant adhesin was obtd. by expression of the encoding sequence (see AR10105) in E. coli HBIOI (past). The adhesin can be used as a vaccine for immunisation of cattle against disease or colonisation of mucosal surfaces by O157:H7, thus increasing the safety of food
 Gaps
 9 RINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPA 68
 epithelial adhesin -
a vaccine to prevent
 38 KLTNAAASVSVISQEELQSSQYHDLAEALRSVEGVDVESGTGKTGGLEISIRGMPASYTL
 KRPTKAFQGHAAAG-----FGTHKQYK----AEADVSGSLNSDGSVRGR-----V
 275 LPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKL
 G------YLNW
 395 RSTNEOGRITLYA-----RGGLALNEPRSIPOVDLIANA-RKGVRGYSHTVA----
 366 SMKDGVVLASTGETFRQKSWSVFAEDEWHLTDALALTAGSRYEHHEQFGGH-----
 7.8%; Score 294.5; DB 17; Length 696; ilarity 20.7%; Pred. No. 1.7e-17; Conservative 103; Mismatches 302; Indels 255;
 RITTLASVVIPCLGFS--ASSIAAABDVMIVSASGY----EK-
 Chromosomal DNA from E. coli 0157:H7 encoding isolated on plasmid pSC (overlap), for use as bacterial colonisation of bovine intestine
 CHILDREN'S HOSPITAL & MEDICAL CENT.
UNIV WASHINGTON.
UNIV WASHINGTON STATE RES FOUND.
 Disclosure; Page 31-32; 42pp; English
 Tarr PI,
 95WO-US06994
 94US-0265714
 Bilge SS,
 1996-068826/07.
 derived from cattle
 Best Local Similarity
Matches 172; Conserv
 696 AA;
 N-PSDB; AAT10105
 07-JUN-1995;
 24-JUN-1994;
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 Sequence
 Query Match
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 The invention relates to the identification of iroNec gene, from an extraintestinal isolate of Escherichia coll. This gene is expressed in increased amounts in human urine and is identified by transposon (TnphoA) mutagenesis. iroNec gene
 Novel isolated iroNec polynucleotide from extraintestinal isolate Escherichia coli useful as vaccine for treating or preventing extraintestinal infections caused by extraintestinal pathogenic
 Misc-difference
 meningitis;
 E. coli iroNec
 AAY72914;
 AAY72914 standard;
 Claim
 Misc-difference
 Escherichia coli
 13-JUN-2001
 Escherichia
 22-SEP-1999;
 22-SEP-2000; 2000WO-US26117
 29-MAR-2001
 WO200121636-A1
 Protein
 iroNec; extracytoplasmic protein; immunogen; vaccine; immunotherapy; extraintestinal infection; urinary traingitis; pneumonia; intra-abdominal infection; ant
 (UYNY) UNIV NEW YORK STATE RES
 Peptide
 647
 689
 646
 530
 590
 475
 532
 417
 --FSPRAYLVMDVADAWTLKGGVTTGYKAPRMGQLHKGISGVSGQGKTNLLGNPDLKPEE
 2001-244936/25
 NLLNKDYSDVSLYSAGKSTLYAGDYFQTGSSTTGYVIP--ERNYWMSLNYQF 696
 FAGTL-PLWSEDVTLSLNYTWTRSEQRDGDNK--GAPLSYTPEHMVNAKLNWQITEEVAS
 NI FNRHY - - -
 WLGARYRGKTPRFTQNYSSLSAVQKKVYDEKGEYLKAWTVVDAGLSWKMTDALTLNAAVN
 GGGV-----
 ISGAVTPKWQ----IHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQVTPELTI
 SVSYEAGV---YYDNPAGLNANVTGFMTDFSNKIVSYSINDNTNSYVNSGKARLHGV--E
 GNOFEVGYKGSYMDD---RINARVSFYRMKDKNAAAPINPNNKKTRYAALGKRVMEGVETE
 9
 'n
 AAD03054.
 Page 39-41; 44pp;
 Carlino
 coli
 (first
 99US-0155621
 extracytoplasmic protein fragment
 120..
 /label= Signal_peptide
25..725
 Location/Qualifiers
 'note=
 note= "Encoded by
 label = Mature_E. coli_iroNec_extracytoplasmic_protein
 ----NAMSGITSSA----GMHAGGYATFDAMAAYRFTPKLKLQINAD
 Protein;
 entry)
 . 121
 "Encoded
 English.
 725
 protein.
 YARVGGANT - FNI PGSERTWTANLRYSF
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 AAC TGG"
gene
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 573
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 469
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Matches
 Query Match
Best Local
 comprising nucleotide sequence encoding one or more antigenic epitope of iroNec is useful for diagnostic and immunotherapeutic purposes. The iroNec antigenic peptide is useful for treating or preventing extraintestinal infections (EIs) caused by extraintestinal infections (EIs) caused by extraintestinal pathogenic E. coli (ExPEC). The EIs include urinary tract infection (UTI), meningitis, intra-abdominal infection
 Sequence
 an immunogen in vaccine formulations.
 461
 216
 212
 117
 99
 40
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 present sequence
 pneumonia
 LSQELGDYFKVKAGVARTFKAPNLYQSSE----GYLLYSKGNGCPKDITSGGCYLIG---
 RGRV-----MAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLG--AGYLYQQRH
 MSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGT
-SGKELGAYSLVGTNFNYDINKNLRLNVGVSNILNKQIFRSSEGANTYNEPG--RAYYAG
 SAGMHAGGYATFDAMAAYRFTPKLKLQINADNI FNRHYYARVGGANTFNI PGSERTWTAN
 PLSVIPKYTINNSLNWTITQAFSASFNWTLYGRQKPRTHAETRSEDT
 FL-LMPKHSAN------LWTTY-----QVTPELTIGGGVNAMSGITS
 TASGAYILKWONGGKALVDGIEASMSFPLVKERLNWNTNATW-----MITSEOKDTGN
 TRYAAL-----GKRVMEGVETEISGAVTPK---WQIHAGYSYLHSQIKTASNSRDDGI
 LYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKK
 ANARKGVRGYSHTVATENLDEF-GIYGKSTFHPADGLSLIGGGR--------
 SWRTSGELNIPLNVMVDQTLTVGAEWNRDKLDDPSSTS-----LTVND-RDI-----
 PFRLGNTAN-----EFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLI
 GVYYEKTN-----NTRMNEGLSGGGEGRILAGEK------FTTNRLS
 GMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSR
 ----NIYAGDTONSSSAVTESLAKSGKETNRLYRONYGI----TH---NGIWDWGQSRF
 LAPYNGLPADANNKLPSLPQHVFV--GADWNKFKMNSHDVFADLKHYFGNG----GYGKV
 YGNLNKTDADSWDINSPYGTKNAAGHEGVRNKDINGVVSWKLNPQQILDFEVGYSRQG--
 SGAAGGVVNIITKRPTNDW--HGSLSLYTNQPESSEEGATRRANFSLSGPLAGDALTTRL
 SGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEA-----DVSGSLNSDG---SV
 GMGPENTLILIDGVPVTSRNSVYSWRGERDTRGDTNRWVPP-EQVERIEVIRGPAAARYG
 ARGYEYSEYNIDGLPAQMQS---
 TAEQVLKQQP-GVSVITSEDIKKTPPVNDLSDIIRKMPGVNLTGNSASGTRGNNRQIDIR
 KIPASLREIPQSVSIITNQQVKDR-NVDTFDQLARKTPGLRVLSN-----DDGRSSVY
 MRINKILWSLTVLLVGLNSQVSVAKYSD---
 167;
 ----NKDLD----
 ----SGISGSAADRSSKNHSQISALYIEDNIEPVPGTNIIPGLRFDYLSDSGGNFSPSLN
 Similarity
 LGHY-KIESGEGKT-----LHKASKTKFTGYA-----GAVYDLNDNNSLYLSLSQ
 725 AA;
 Conservative
 7.2%;
 8
 PEISVNKEIGLEFTWED--YHASVTYFRNDYQNKIVAGDNVIGQ
 E. coli iroNec extracytoplasmic
 127;
 Score :
 -----INGTLPNLFAFDRVEVMRGPSGLFDS
 Mismatches
 e 273.5;
 The recombinant vector
 .5e-1
 BG
 304;
 22;
 Indels
 Length
 -DDNDETLVVEA 39
 protein
 247;
 Gaps
 425
 622
 572
 460
 162
 116
 717
 663
 657
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 513
 512
 468
 404
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 374
 322
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 215
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PSLPQHVFVGADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKL 334
 21-MAR-2001; 2001WO-US09180
 2000US-191078P.
2000US-206848P.
 2000US-207727P.
 2000US-242578P.
2000US-253625P.
 2000US-257931P
 2001US-269308P
 (first entry)
 Ohlsen KL,
Xu HH;
 PHARM INC
 Pseudomonas aeruginosa.
 WPI; 2001-611495/70.
 N-PSDB; AAS51448
 478 YASYNKGFAP-
 WO200170955-A2.
 (ELIT-) ELITRA
 567 NPNNK 571
 511 TPNTK 515
 21-MAR-2000;
 26-MAY-2000;
 23-OCT-2000;
 16-FEB-2001;
 Haselbeck R,
 Yamamoto RT,
 23-MAY-2000;
 27-NOV-2000;
22-DEC-2000;
 14-FEB-2002
 27-SEP-2001
 AAU33589;
 335
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 25;
 The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dabA, fhaB, fhuB, rni5, rhl17, rhl18, rth19, rth20, rth21 and tolc genes. These can be used in the diagnosis and treatment of infection by the bacterium, which can lead to meningitis and bacteraemia, and in vaccines to prevent
 Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
 VTRNGQL---IKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFLRG 116
 VTVGTKIPASLREIPOSVSIITNOQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG 119
 TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGASPR 225
 PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAP-----YN--GLPADANNKL 275
 233 ITVKLDN-----GLKWT-----GQYTYDNVERTPDRSPTKSVYDRFGLPYRMGFAH 278
 120 YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
 Gaps
 5 FHLALLPTLIA--SPPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA 60
 8 FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA 59
 Meningococcus; meningitis; bacteraemia; vaccine; dsbA; fhaB; fhuA;
 135;
 DB 22; Length 697;
 6.4%; Score 241.5; DB 22; Length 20.8%; Pred. No. 1.2e-12; tive 99; Mismatches 245; Indels
 T SANTE & RECH MEDICALE.
FOERDERUNG WISSENSCHAFTEN
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 Neisseria meningitidis protein #23
 Claim 3; Fig 23B; 240pp; English.
 AAB68924 standard; Protein; 697
 99EP-0401764
 99EP-0401764
 (first entry)
 Best Local Similarity 20.8
Matches 126; Conservative
 (INRM) INSERM INST NAT
(PLAC) MAX PLANCK GES F
 Neisseria meningitidis
 Tinsley C;
 2001-082916/10.
 697 AA;
 N-PSDB; AAF56464
 rth; told
 725
 such infection
 EP1069133-A1
 13-JUL-1999;
 13-JUL-1999;
 18-APR-2001
 17-JAN-2001
: ||
VTASF
 Nassif X,
 AAB68924;
 Seguence
 Query Match
 rni5;
 721
 09
 178
 173
 61
 226
 RESULT 31
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
P-----NDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSEN 326
 327 GSRIKRNYAWQQT------DNKTLSSNFTLNGDYTIGRFENHLTVGMDYSR- 371
 RSTNEOGRITLYARGGLALNEFRSIPOVDLIANARKGVRGYSHTVATEN---LDEFGIYG 451
 YLSLSQLYTPQTNLDADGKLLKPROGNOFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPL 566
 -----YGGRGYLSIDTSSAAVF-----NAAPEY 510
 ß
 GMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRF
 KSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA-----GAVYDLNDNNSL
 Carr
 of•
 Trawick JD,
 polynucleotides for the identification and development thinging comprise sequences of antisense nucleic acids
 Pseudomonas aeruginosa cellular proliferation protein #33.
 Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
 antibiotics, comprise sequences of antisense nucleic
 Zyskind JW, Wall D,
 Example 3; Seq ID No 5085; 511pp; English
 Š
 AAU33589 standard; Protein; 813
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Matches
 Query Match
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 pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
 Sequence
 ftp.wipo.int/pub/published_pct_sequences
 607
 563
 475
 430
 374
 393
 324
 353
 274
 296
 246
 186
 196
 129
 158
 107
 525
 506
 723
 77
 19
 Local Similarity
 VGASYDAHGDRIAPEPSQGDLFDSN----VYNIGGKLGLRIDENQRVQLALSHYDARQDTD 352
 GVPLNTNRDSGRNLANIDPALIERIEVIRGSSAIY-GSGATGGIIS-ITTRP-----
 VSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSE-----YNID 128
 AALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIP-ASLREIPQ-S
 SNLEPVKTNNYELGWRGAIGGNTLGSLALFYTTSKLGDVQSFNNGLILTR----TKERIY
 RPFRLGNTAN-EFVIGADYNRFRS---TNEQGRTTLYARGGLALNEFRSIPQVDLIANAR
 AAADWDINPDTVL---GAGYLYQQRHLAPYN----GLPADANN------
 DSLAT-----EYGQTLRGRSMLVMVD
 KLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVME 584
 YATDPRVARLPPGSVPANAIKGLELDE-QNRIRNTLANLEY----------
 AAGFGTHKQYKAEADVSGS-----LNSDGSVRG---RVMAQTVGASPRPAEKNNRHETFY
 GLPAQM-QSINGTLPNL--FAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHA 185
 NNRLQATFFDSKDY--
 NSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAY
 GVEASADWLSDDEVWGAGGSATWMRGREKPDGKDWQDMTGYRVPPLKLTAYLQYKPDADW
 GVE---
 ESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLS-----QLYTPQTNLDADG
 AGAFAQLQHRFDEHWSIDGGLRYEYSTAEFDDFIPLSES---KAASPVTVKGGDLDYDAV
 LRTPLGESGNTELVWGGDYNQERSDMPLDVFDPAAYDASGGLVFDKIGKLTYMPPLRTRS
 -ENLDILGSRLSAQLYYRDYFTRFTPFDARAVSTRG-----GNVDQIMQNSEVFGSRLT
 DSNYAFAGSKLGMK-----
 AGG----ENRAETRLSATSPLTRLGSDG-LGGQFQQYFAGSLGALDYSFDFGTRH----
 AAVPATOARSEPLDMEQMEITASRTSSDLVS-----ATROSTVIEHAQLEELROGS
 -----KLP--SLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDA
 813 AA;
 Conservative
 6.3%;
 ---LGIVYSPVAGQEIYASFSQGFQLPDVGIQLRNARRGFDIGS
 -RGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKI 474
 107;
 TEISGAVTP---KWQIHAGY-----SYLHSQIKTAS
 Score 237.5;
Pred. No. 3.5
 -TPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYS
 Mismatches 301;
-----RLDGVESFGRRQVSTYTTVDLVSQY
 .5e-12
 DB 22;
 Indels
 Length
 253;
 813;
 Gaps
 505
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 infections, such as meningitis, septicaemia and gonorrhea. Bo organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
 Sequence
 their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria
 Claim 4; Page 379; 524pp; English
 Proteins from Neisseria meningitidis and diagnosis, treatment and prevention of ir
 Grandi G,
 and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORFs) AAZ11972-Z12358. The antigenic proteins,
 Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis
 N-PSDB; AAZ12258
 27-NOV-1997
 06-NOV-1997
 01-SEP-1998;
 09-OCT-1998;
 W09924578-A2
 Neisseria meningitidis
 treatment;
 Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 Neisseria meningitidis antigen
 08-OCT-1999
 AAY38830
 14-JAN-1998
 111
 18-NOV-1997
 14-NOV-1997
 (CHIR-) CHIRON SPA.
121
 171
 762
 676
 231 NRHETFYAAADWDINPDTVLGAGYLYQQRHL---APYNGLPADANNKLPSLPQHVFVGAD
 61
 Local Similarity
 1999-327407/27.
SRXAELYGILEYDIAPQTRVHAXMDYQQAKETADAPLSYAVYDSQGYATAFGPKDNPATN
 NLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKN 230
 GRSSVYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIV 170
 RITPDDQLSLGIQNLFNRDYYPLYSQLLRNNNNTSHLPAPGTVLTASYTHNW
 GYNYLFARGSRIANYQINGIPVADALADTGNANTAAYERVEVVRGVAGLLDGTGEPSATV
 RFTPKLKLQINADNIFNRHYYARV-----GGANTFNIPGSERTWTANLRYSF 722
 standard; Protein;
 Masignani
 Neisseria infection; meningitis; septicaemia; gonorrhea.
 211 AA;
 Conservative
 (first entry
 97GB-0026147
98GB-0000759
 98WO-IB01665
 97GB-0025158
 97GB-0024386
 97GB-0024190
 97GB-0023516
 98GB-0019016
 6.2%;
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 and prevention
 Pizza
 34; Mismatches
 211 AA
 Score 235.5; DB Pred. No. 6.2e-13
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 encoded by a partial
 Rappuoli
 N. gonorrhoeae useful
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 Scarlato V;
 Indels
 Length
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 Gaps
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11-FEB-2002
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 13-SEP-2001
 ABB52836;
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 37;
 The invention relates to a library of DNA fragments of Escherichia colistrains comprising polynucleotides (ABA8877-ABA88729 and ABA89533) and encoded proteins (ABB524959-ABB52914) and encoded proteins (ABB52919-ABB52914) of nature B2/D+A-. The polynucleotides have potential antiinflammatory, antibacterial and immunosuppressive activity as part of pharmaceutical compositions used to treat, pallate or prevent extra-intestinal E. coliinfections. The polypeptides are useful for determining the phylogenic group of a given E. coli strain. These polypeptides can detect and treat an undesired development of E. coli, particularly an extra-intestinal infection that include systemic and non-diarrhoeal infections such as septicaemia, pyclonephritis and meningitis this is particularly advantageous as bacterial resistance is increasing with the more frequent use of broad spectrum antibiotics.
 A library of DNA fragments of Escherichia coli strains for the phylogenic determination of a given strain comprises polynucleotides of
 Escherichia coli; B2/D+A-; antiinflammatory; antibacterial; immunosuppressive; extra-intestinal infection; phylogeny; meningitis; systemic infection; non-diarrhoeal infection; septicaemia; pyelonephritis; antibiotic resistance.
 120 YEYSE--YNIDGLPAQMQS--INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIV---- 170
 GTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSS----VYARG 119
 Gaps
 3 QFMSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTV 62
 ------EAPMMVSVIDTSAPENQTATSATDLLRHVPGITL--DGTGRTNGQDVNMRG 93
 Query Match 6.0%; Score 228; DB 22; Length 660; Best Local Similarity 19.7%; Pred. No. 1.8e-11; Matches 157; Conservative 107; Mismatches 276; Indels 258;
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 Nassif X,
 (INRM) INSERM INST NAT SANTE & RECH MEDICALE
 Escherichia coli polypeptide SEQ ID NO 732.
 Clermont O,
 ABB52669 standard; Protein; 660 AA
 Example 6; Fig 6; 646pp; English.
 WNKFKMNSH----DVFADLKHYF 306
 12-MAR-2001; 2001WO-EP03445.
 2000FR-0003145
2001FR-0001449
 (first entry)
 Bonacorsi S,
 WPI; 2001-550253/61.
 660 AA;
 Escherichia coli
 phylogenic deter
nature B2/D+ A-
 WO200166572-A2
 10-MAR-2000;
02-FEB-2001;
 11-FEB-2002
 13-SEP-2001
 Bingen E,
 ABB52669;
 Sequence
288
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94 YDHRGVLVLVDGVRQGTDTGHLNGTFLDPALIKRVEIVRGPSALLYGSGALGGVISYDTV 153
 ---NLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSV-----RGRVMAQTVG 221
 154 DAKDLLQEGQSSGFRVFGTGGTGDHSLGLGASAFGRTENLDGIVAWSSRDRGDLRQSNGE 213
 214 TAPNDESINN-----MLAKGTWQIDSAQSLSGLVRYYNNDAREPKNPQTVEASD---SSNP 266
 267 WDRSTIQRDAQLSYKLAPQ----GNDW------LNADAKIY-----WSEVRINAQN 308
 381 TANEFVIGADYNRFRSTNEQGRTTLYARGGLALNE------FRSIPQVDLIANAR-KG 431
 VRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFT 491
 492 GYA------GAVYDLNDNNSLYLSLSQLYT----PQTNLDADGKLLKPRQGNQFEVGY 539
 477
 540 KGSYMD-----DRLNARVSFYRMKDKN------AAAPLN---PNNKKTRYAALGKRV 582
 MEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQVTPE 642
 LTIGGGVN---AMSGIT-----SSAGMHAGGYATFDAMAAYRFTPKLK--- 682
 Escherichia coli; B2/D+A-; antiinflammatory; antibacterial; immunosuppressive; extra-intestinal infection; phylogeny; meningitis; systemic infection; non-diarrhoeal infection; septicaemia; pyelonephitis; antibiotic resistance.
 222 ASPRPAEKNNRHETFYAAADWDI--------NPDTVLGAGYLYQQRH
 LAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSD
 321 RDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGN
 309 TGSSGEYREQITK---------GARLENRSTLFADSFA----
 YRGSSDGYKDVDADKWSSRAGMTINPTNWLMLFG-----
 533 MTKYTTDL------SSLDVAYN-----RTRGKDTDTGEYI------SSINPD
 Escherichia coli polypeptide SEQ ID NO 1077.
 Ė
 682
 12-MAR-2001; 2001WO-EP03445.
 ABB52836 standard; Protein;
 10-MAR-2000; 2000FR-0003145.
02-FEB-2001; 2001FR-0001449.
 644
 (first entry)
 683 LQINADNIFNRHYYARVG
 627 TTLVLGNAFDKEYWSPQG
 WO200166572-A2.
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 B2/D+A. The polynucleotides have potential antinflammatory, antibacterial and immunosuppressive activity as part of pharmaceutical compositions used to treat, palliate or prevent extra-intestinal E. coli infections. The polypeptides are useful for determining the phylogenic group of a given E. coli strain. These polypeptides can detect and treat an undesired development of E. coli, particularly an extra-intestinal infection that include systemic and non-diarrhoeal infections such as septicaemia, pyelonephritis and meningitis this is particularly advantageous as bacterial resistance is increasing with the more frequent use of broad spectrum antibiotics.
 Sequence
 and encoded proteins (ABB52459-ABB52919 and ABB52954-ABB53094) of nature
 The invention relates to a library of DNA fragments of Escherichia colistrains comprising polynucleotides (ABA88577-ABA88729 and ABA89533)
 Example 6; Fig 6; 646pp; English
 nature B2/D+ A-
 A library of DNA fragments of Escherichia coli strains for the phylogenic determination of a given strain comprises polynucleotides
 (INRM) INSERM INST
 436
 509
 391
 453
 348
 356
 244
 297
 237
 164
 181
 105
 133
 Local Sin
hes 159;
 49
 75
 12
 5
 GLGTEI ----
 DVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTP-AGRPGCNTADDKACAV 355
 ASVSVITSEQLQKKPVSDLVDAVKDVEGISITGGNE-KPDISIRGLSGDYTLILVDG---
 ATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIP 74
SFYRMKDKNAAAPLNPNNKKT-----RYAALGKRVMEGVETEISGAVTPKWQIHAGYS
 GIAKAFRAPSIREVSPGFGTLTQGGASIMYGNRDLKPETSVTEEIGIIYS-NDSGFSASA
 RSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATE--NLDEFGIYGK 452
 QTWDGVLGLGGIIQEHGKF-----GNSTTNDFYLSGPLIKDKLGLQ--
 NEYAATDSLALTGGLRLDNHEI --
 LPEN-----TTETQSVSIKQKAVFIE
 NAQGEILHPEIAVYQEKVIREVKSGKKDKYNHWDLNYESRKPEITNT----IIDAKVTAF
 -VFE-----YGKNNOVHTLTPGESLDAWT-MRGNLKOPNSKRETHNSRSHWVAAW
 YAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSH
 RRQSGRESRPNGSGGFEAGFIPPVEAIERIEVIRGPMSSLYGSDAIGGVINIITK-PVNN 163
 QMQSIN----
 AVMCSAVISSGYASSDKKEDTL-------------------VVTASGFTQQLRNAP
 2001-550253/61
 SLSQLY-TPQTNLDADG-----
 STFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAG----AVYDLNDNNSLYL
 FQGHAAAGFG----THKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETF 236
 QSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGY--EYSEYNIDGLPA 132
 Similarity
 682
 Conservative
 ---LYGGMNYRKED-SISQGTPAKDNKNITATLQ--FTPTESQKF-----
 NAT
 5.9%;
 ß
 -GTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA 180
 -----KOKALAFDASY-SRPFRLGNTANEFVIGADYNRF 394
 SANTE & RECH
 Clermont 0,
 116;
 Score 222.5; DB 22;
Pred. No. 6.2e-11;
 Mismatches
 ---KLIKPROGNOFEVGYKGSYMDDRLNARV
 MEDICALE
 Nassif X,
 ---YGSYWNPRLYAVYNLTDNLTLKG
 Tinsley
 Indels
 Length
 682;
 203;
 Gaps
 291
 605
 243
 204
 48
 435
 347
 0f
 33;
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RESULT 36
AAY80096
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 molecules can degrade or transport fumonisin and can reduce the pathogenicity of a fungus producing fumonisin. The plants may be e.g. maize, sorghum, wheat, tomato, soybean, alfalfa, sunflower, Brassica, cotton or rice. The products can also be used as detection reagents for fumonisins and related compounds. AAS91253 represents the Bacterium 2412.1 fumonisin catabolic gene cluster, and AAS91254 to AAS91273 represent isolated nucleic acids from Bacterium 2412.1 which encode AAY80085 to AAY80104. AAZ91286 to AAS91291 represent sequence used in the exemplification of the present invention. AAZ91274 to AAZ91285 are given in the sequence listing from the present specification but are not specifically mentioned further.
 The present invention describes isolated nucleic acid molecules which encode fumonisin degradative enzymes and transporters from a Bacterium 2412.1 fumonisin catabolic gene cluster. The Bacterium 2412.1 was isolated from maize. The nucleic acid molecules can be used for producing an enzyme for detoxifying fumonisin or a structurally related mycotoxin, e.g. in harvested grain, or processed grain which is to be used as animal feed or silage. Ruminal microorganisms transformed with the nucleic acid molecules can be used as probiotic compositions or as feed inoculant compositions. Plants transformed with the nucleic acid
 New isolated nucleic acid molecules which encode fumonisin degradative enzymes and transporters, used for detoxifying fumonisin or related mycotoxin or reducing the pathogenicity of fungi producing fumonisin
 Claim 1;
 N-PSDB; AAZ91265
 WPI; 2000-171270/15.
 Duvick JP,
 15-JUL-1998;
 14-JUL-1999;
 Bacterium 2412.1.
 Bacterium 2412.1; maize; detoxification; degradation; carcinogen;
 TonB dependent receptor
 16-MAY-2000
 AAY80096;
 AAY80096 standard; Protein;
 27-JAN-2000
 (PION-) PIONEER HI-BRED INT INC.
 673
 712
 613
 909
 495
 RYW-ANVRVSF
 RTWTANLRYSF
 GMHAG-----GYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSE 711
 YLHSQIKTASNSRDDGIFL-----LMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSA 659
 TLFNTDFKNKLTSYDIGTKDPVTGLNTFIYDNVGEANIRGVELATQIPVYDKWHVSANYT
 AQRNGAKVPRVRNGFTSMDIGLNYQILPDTLINFAVLNVTDRKSEDIDTIDGNWQVDEGR
 FTDSRRKSDDESL-NGKSLKGEPLERTPRHAANAKLEWDYTQDITFYSSLN-YTGKQIWA
 Page 148-151; 181pp; English.
 catabolic gene cluster;
 Maddox J,
 (first entry)
 99WO-US15837
 98US-0092953
 722
 fccL
 785
 amino acid sequence
 B
 antifungal; mycotoxin.
 SEQ ID
 NO:25
 612
 554
 in the
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us-09-889-267-2.rag

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Grandi G,
Rappuoli R,
 98US-0083758.
98US-0098894.
98US-0098094.
98US-0103749.
98US-0103794.
98US-0103794.
 99WO-US09346
 51; Conservative
 INST GENOMIC RES
 Petersen J, Pizza M,
Tettelin H, Venter JC;
 Galeotti C,
 Neisseria meningitidis
 WPI; 2000-062150/05.
 Best Local Similarity
Matches 51, Conserv
 188 AA;
 N-PSDB; AAZ54298
 CHIRON
 188
 VRKR 176
 09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
 W09957280-A2
 30-APR-1999;
 11-NOV-1999
 01-MAY-1998
 02-SEP-1998
 02-SEP-1998
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IRKR
 Fraser C,
 Sequence
 Query Match
 (CHIR)
 (GENO-)
 61
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 121
 173
 185
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 32;
 373
 352 ADYEVGPVTLTSISAFTHSK----KSGPDDADGTSDSLLHATYGVRSDTWTQEFRAAYS 406
 513
 572
 622
 167
 215 VMAQTVGASPRPAEK-----NNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPY-NG 266
 267 LPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSD--RDAD 324
 374 RPFRLGNTANEFVIGADYNRFRSTNEQGRTTLY---ARGGLAL----NEFRSIPQVDLIA 426
 GQ-RL-----HWVAGAYYLDETLKQNQPLSIFYDGDRFGGLGIPARAGAFDGIAQKSLSQ 460
 NARKGVRGYSHTVATENLDEFGI-----YGKSTFHPADGLSLIGGGRLGHY----KIE 475
 461 NTOKTRSIAAFGQADYTLDRFTLTLGGRYTHERKTFDHFSATQVQAGG-LGKYGPLGKIV 519
 624
 684
 ----FILMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAYRFT 678
 EGKOFHLADDDSVNV-----AFTSAYKSHOFFDSTNAPYTQQEGYWVHNASLTFNSR 736
 ASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRV-LSNDDG-RSSVYARGYEYSEY 125
 -----NSDGSVRGR 214
 LTGGSASGTDNQAVRLQLLYRPNDRLKVLLSSAYGHVNSPIV-----QYRHLGAFAAG 298
 299 TOSSASPILCS-PEQVRAGGCVNVFGAGTPSGF----YDGSSDRGE-RLRVENFLOOAR 351
 514 YTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNAR-VSFYRMKDK-----NAAAPLN 567
 9 RINMTAATVLAALSSSVFA-AQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIP 67
 29 RIMITAAGSALVIGLAPKALAQVAVPPAGHEASQEVQEIVVTAQ------RRS 75
 NIDGLPAQMOSINGTLPN------LFAPDRVEVMRGPSGLFDSSGEMG
 SNY------AFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKOKALAFDASYS
 ---GEGKTLHKASKTKFTG--YAGAVYDLNDNNSLYLSLSQL
 520 SLSEAFKASDPTWRAALSYRPAERVMVYGSVATGFKGGAFNGGFLSSNPNKAL----
 TVTGPVTVTTNVLTNARKAHSQGVELEVKAVPIPDLVLSLQPAWLRTRLDEAGFSGGTSL
 ----PNNKKTRYAALGKRV-MEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGI
 Neisseria meningitidis ORF 743 protein sequence SEQ ID NO:2546
 Query Match 5.8%; Score 220; DB 21; Length 76
Best Local Similarity 20.3%; Pred. No. 1.3e-10;
Matches 162; Conservative 109; Mismatches 345; Indels
 168 GIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSL--
 $
 AAY75536 standard; Protein; 188
 NHWDVGFNVRNLTGTKYY 754
 679 PKLKLQINADNIFNRHYY
785 AA;
 S----S
Sequence
 AAY75536
 126
 325
 568
 737
 92
 246
 407
 427
 476
 573
 623
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AAZ51015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY5941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves may also be used in gene therapy protocols.
Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
 Σ
 TVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGY 120
 EYSEYNIDGLPAQMQSING-----TLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNL 172
 FRINMTAATVLAALSSS-----VFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAV 60
 Masignani V, Mora M;
Scalato E, Scarselli
 Novel Neisserial polypeptides predicted to be useful antigens vaccines and diagnostics
 Length 188;
 Indels
 5.6%; Score 213; DB 21; 27.7%; Pred. No. 5.8e-11;
 യ് യ
 42; Mismatches
 Hickey 1
Ratti (
 Page 1211-1212; 1453pp; English.
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 Query Match
Best Local :
 31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodis and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polypucleotides of the invention may also be used in gene therapy protocols.
 AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
 Claim 2;
 Novel Neisserial polypeptides predicted vaccines and diagnostics -
 Fraser C,
 09-OCT-1998;
 01-MAY-1998;
 30-APR-1999;
 11-NOV-1999.
 WO9957280-A2
 Neisseria meningitidis
 Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septi
 Neisseria
 21-MAR-2000
 AAY75535;
 AAY75535 standard;
 09-OCT-1998;
 (GENO-)
 (CHIR)
 59
63
 σ
 8
 2000-062150/05.
RMSTATGMR I AGKDTPQSVSVITRSRLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFLSR
 AVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYAR 118
 FRINMTAATVLAALSSS------VFAAQTADLETVHIKGQRSYNAIV--TEKNGDYSSF
 FSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGS---HALLGKTEKTRSYTID 62
 Similarity
 CHIRON CORP.
INST GENOMIC RES
 Page 1211; 1453pp; English
 meningitidis ORF
 Galeotti C, Grandi G,
Pizza M, Rappuoli R,
 187 AA;
 Conservative
 Venter JC;
 (first entry)
 98US-0103749.
98US-0103794.
98US-0103796.
99US-0121528.
 gene therapy
 98US-0099062
 98US-0094869
98US-0098994
 99WO-US09346
 Protein;
 5.4%;
27.6%;
 43;
 743 protein sequence SEQ ID NO:2544.
 187
 Score 205; DB 21;
Pred. No. 3.1e-10;
 Mismatches
 B
 Hickey
Ratti
 to be useful antigens
 ១ធ
 Masignani V, Mora M;
Scalato E, Scarselli
 Length 187;
 Indels
 septicaemia;
 20;
 Gaps
122
 58
 3
 4;
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RESULT 39
AAU29336
ID AAU29
XX
AC AAU29
XX
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 Query Match
Best Local Similarity
Matches 170; Conserv
 a newly identified mar regulated (NIMR) polypeptide activity. The method comprises contacting an NIMR polypeptide with a test compound under interaction conditions, determining the ability of the compound to modulate the activity or expression of the polypeptide, and selecting the modulators. NIMR nucleic acids and polypeptides are used in the treatment of microbial infections, and in screening for modulators of NIMR expression and activity. These modulators can be used to reduce the infectivity of a microbe on a surface, and the virulence of a microbe in a subject suffering from an infection. AAU29329-AAU29379 represent Escherichia coli NIMR amino acid sequences of the invention.
 Sequence
 Escherichia coli.
 The invention
 Disclosure; Page 184-187; 526pp; English.
 Identifying compounds that modulate a newly identified mar regulated polypeptide activity, useful as antimicrobial compounds, involves contacting the polypeptide with a test compound -
 N-PSDB;
 Levy
 10-MAR-2000; 2000US-188362P.
 08-MAR-2001; 2001WO-US07478
 27-SEP-2001.
 mar regulated polypeptide; NIMR; microbial infection; antibacterial
 Novel mar regulated protein
 18-DEC-2001
 AAU29336 standard; Protein; 774
 183
 171
 123
 119
 56
 79
 79
 24
 18
 NLIRK 187
 2001-602769/68.
 NLVRK 175
 GFYIDQIGEDGMTVNVAGRSGYTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGGTV 182
 GYEYSEYNIDGLPAQMQSING--
 IITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYN-----ID 128
 LAALSSSVFAAQ--------TADLETVHIKGQRSYNAIVTEKNGDY- 55
 VESGLQQLLDGSGLQVKPLGNNSWTLEPAPAPKEDALTVVGDWLGDARENDVFEHAGARD 138
 LAGLSFSAFAAQVNIAPGSLDKALNQYAAHSGFTLSVDASLTRGKQS-NGL----HGDYD
 AAS46238
 TUFTS COLLEGE
 Barbosa TM,
 774 AA;
 Conservative 108;
 (first entry)
 relates to a method of identifying compounds that modulate ified mar regulated (NIMR) polypeptide activity. The method
 5.4%;
::
 Alekshun
 (NIMR) #8
 Score 205; DB 2
Pred. No. 3e-09;
08; Mismatches 3
 -TLPNLFAFDRVEVMRGPSGLFDSSGEMGGIV 170
 -SSFAVTV----
 316;
 22;
 Length
 GTKIPASLREIPQSVS 78
 Indels
 250;
 Gaps
 78
 39;
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438
 IP-----QDFGIEAGVEGQLSPTSS------QNNPKETHNLMV 283
 SDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKOKALAFDASYSRPFRL 378
 494
 604
 SYLHSQIKTASNSRDDGIFLLMPKHSANL------WTTYQVTPELTIGGGVNAMSGIT 656
 SSAGMHAG---GYATFDAMAAYRFTPK---LKLQINADNIFNRHYYARVGGANTFNI-PG 709
 VIRREDFAKTGATTMREVLNRIPGVSAPENNGTGSHDLAMNFGIRGLNPRLASRSTVLMD 198
 -------FYA---AADWDIN-----PDTVLGAGYLYQQRH-----LAPYNG---L 267
 GGTADNGFGTALLYSGTRGSDWREHSATRIDDLMLKSKYAPDEVHTFNSLLQYYDGEADM
 GNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHT
 439 VATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGK----TLHKASKTKFTGYA
 : : : | | : | | : | | : | | EMGLELINFNN---QYDSNQTNDTVTARGKTRHTGLETQARYDLGTLTPTLDNVSIYASY
 GLPA------QMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA
 FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHET----
 ----YLDDKIDIGNWTITP-----GMRFEH--IESYQNNAITGTHEEVSYNAPLPAL
 GAVYDLNDNNSLYL----SLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNA
 RVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEIS---GAVTP---KWQIHAGY
 PA-----DANNKLPSLPQHVFVGADWNKFKWNS--HDVFADLKHYFGNGGYGKVGMRY
 Human, chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
 Novel human diagnostic protein #17851.
 ABG17860 standard; Protein; 454 AA
 31-MAR-2000; 2000US-0540217
 30-MAR-2001; 2001WO-US08631
 (first entry)
 WO200175067-A2
 SERT 713
 762 QPŘŤ 765
 Homo sapiens
 18-FEB-2002
 11-OCT-2001
 ABG17860;
139
 284
 129
 199
 181
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (II) as useful as hybridisation probes, polypeptide (II) sequences. (II) as useful in gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques or restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponaitles, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Specification, but was obtained in electronic format directly from MIPO
 LREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVY------ARGY 120
 10KVPOSISVVTAEEMALHQPKSVKEALSYTPGVSV--GTRGASNTYDHLIIRGFAAEGQ 172
 EYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPT-- 178
 SQNNY-LNGLKLQGNPYNDAVIDPYMLERAEIMRGPVSVLYGKSNPGGLLNMVSKRPTTE 231
 PLKEVQFKA----GTDSLFQTGFDFSDSLDDDGVYSYRLTGLARSANAQQKGSEEQRYAI 287
 Gapa
 288 APAFTWRPDDKTN----FTFLSYFQNEPDTGY-YGWLPKEGTVEPLPNGKRLPTDFNDR 341
 INMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPAS 69
 -----RPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPY-NG--LPADANNK 274
 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
 --KAFQGHAAAGFGTHKQYKAEADVSGSLNSDG--SVRGRVMAQTVGASP-----
 / Match 5.2%; Score 196; DB 22; Length 4 Local Similarity 24.7%; Pred. No. 8.4e-09; Length 4 74; Conservative 52; Mismatches 127; Indels
 invention relates to isolated polynucleotide (I) and
 ftp.wipo.int/pub/published_pct_sequences
 Claim 20; SEQ ID No 48219; 103pp; English.
 AAB40909 standard; Protein; 134
 Tang YT;
23-AUG-2000; 2000US-0649167.
 (first entry)
 WPI; 2001-639362/73
 Liu C,
 454 AA;
 (HYSE-) HYSEQ INC
 N-PSDB; AAS82047.
 08-FEB-2001
 Drmanac RT,
 Seguence
 AAB40909
 Query Match
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 121
 Matches
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 179
 225
 AAB40909
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anticonvulsant; osteopathic; antiarthritic; immunosup; immunostimulant; thrombolytic; coagulant; vasotropic;

immunosuppressant; cardiant; cytostatic; hepatotropic; nootropic; neuroprotective;

Human; open reading frame; ORFX; detection; Human ORFX ORF673 polypeptide sequence

SEQ ID NO:1346

vulnerary; antipsoriatic; antiparkinsonian;

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 CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; cc immunostimulant; cardiant; thrombolytic; coaquilant; vasotropic; cc antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; cc antidialetic; hypotensive; dermatological; antifungal; antirhoumatic; cc antidialetic; and antianaemic. The sequences can be used for determining cc the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The cnucleic acids can be used to express OREX proteins in gene therapy cectors. The proteins and nucleic acids may be used to treat cancers, cc proliferative disorders, neurodegenerative disorders, osteoarthritis, cc profiferative disorders, neurodegenerative disorders, osteoarthritis, cc graft vs host disease, cardiovascular disease, diabetes mellitus, cc proteins on hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, alterias and nucleic and any autoimmune disorders, asthma, alterias anaemia burns woulds browned disorders, asthma, alterias anaemia burns woulds browned disorders.
 hypotensive; dermatological; immunosuppressive; antidiabetic; antianaemic; gene therapy; cancer; proliferative disorder; hyportension; eurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.
 31-MAR-1999;
02-APR-1999;
05-APR-1999;
 Sequence
 allergies, aplastic anaemia, burns, wounds, bone and cartilage damage. nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
 AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
 Claim 11; Page 1152; 5507pp; English.
 Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
 WPI; 2000-602362/57.
 Shimkets RA,
 31-MAR-2000; 2000WO-US08621.
 WO200058473-A2
 Homo sapiens.
457 PADGLSLIGGGRLGHYKIESGEGKT-LHKASKTK--
 CURAGEN CORP.
 Similarity
 134
 Conservative
 2000US-0540763
 Leach
 99US-0127607.
99US-0127636.
99US-0127728.
 3
 39.0%;
 20;
 Score 195; DB 21;
Pred. No. 1.5e-09;
 Mismatches
 38;
 ---FTGYAGAVYDLNDNNS 505
 Length 134;
 Indels
 14;
 frame
 Gaps
 ×
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protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.

The sequence data for this patent did not form part of the printed

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 문
 The present invention describes substantially purified human proteins CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 cc in the specification). ABN15762 to ABN27252 encode the human ORFX CC proteins given in ABP00101 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated CC disorder in humans, and in the manufacture of a medicament for treating a cc syndrome associated with ORFX-associated disorder: ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, cp sociasis, benign tumours, keloid, degenerative disorders related to organ cransplantation, cardiovascular diseases, diabetes mellitus, systemic clupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficitencies and disorders, rheumatoid clarathritis, autoimmune disorders such as multiple sclerosis, rheumatoid crathritis, autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, on preference in the crathron of treating osteoporosis, or periodontal disease, and for gut
 Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
 N-PSDB; ABN22508.
 30-MAY-2000;
29-AUG-2000;
 myasthenia gravis
 degenerative disorder; ostocarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hyperthyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
 Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 Human ORFX protein sequence SEQ ID NO:13494.
 ABP06756;
 ABP06756 standard;
 Disclosure; SEQ ID 13494; 1037pp; English.
 29-MAY-2001; 2001WO-US10836
 WO200192523-A2
 Homo sapiens.
 24-JUN-2002
 autoimmune disorder; rheumatoid arthritis;
 (CURA-) CURAGEN CORP.
 506
 42
 62
 ហ
 2002-106308/14.
 LYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAA 563
 VYTSYTKIYKPQNSKDADRKLLDPIEGDTYEAGLKAAFFDGRLNASFAAFRIEQDNVA 119
 PTDDLSVILGTRVSNF---SGTDNTDFYDPTKADNRLTYRQTGVVTPYAGIVYDLNDIWS
 RA, Leach MD
 2000US-206132P
2000US-228716P
 (first entry)
 Protein;
 134
 ₽
 autoimmune
 61
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26
 646
 Matches
 RESULT 44
 AAY34494
ID AAY3
 8X333X8
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 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving constitutions a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
 3;
specification, but was obtained in electronic format directly from WIPO
 PADGLSLIGGGRLGHYKIESGEGKT-LHKASKTK------FTGYAGAVYDLNDNNS 505
 Gaps
 5 PIDDLSVILGTRVSNF----SGIDNIDFYDPTKADNRLTYRQIGVVTPYAGIVYDLNDIWS 61
 . | | . . . | | | . | | | | | | | | . | . | | | . | . | | | | | . | . | | | | . | . | | | . | . | . | | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | .
 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
 1; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
 506 LYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAA
 14;
 Length 134;
 38; Indels
 5.2%; Score 195; DB 23; 39.0%; Pred. No. 1.5e-09;
 at ftp.wipo.int/pub/published_pct_sequences.
 20; Mismatches
 Claim 20; SEQ ID No 60111; 103pp; English.
 Novel human diagnostic protein #29743.
 Ž
 ABG29752 standard; Protein; 340
 Tang YT;
 30-MAR-2001; 2001WO-US08631
 31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
 46; Conservative
 (first entry)
 Liu C,
 WPI; 2001-639362/73.
 Local Similarity
 134 AA
 (HYSE-) HYSEQ INC
 N-PSDB; AAS93939
 WO200175067-A2
 Homo sapiens.
 biodiversity
 18-FEB-2002
 Drmanac RT,
 11-OCT-2001
 Sequence
 ABG29752;
 Query Match
 457
 food
 Matches
 RESULT 43
 ABG29752
 SXSXS
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4
 AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymons gingivalis (PG) polypeptide sequences given in AAY34318 to AAX91802 to AAX91999 represent PCP primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial
diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 528 KPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVE 587
 588 TEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLL--MPKHSANLWTTYQVTPELTI 645
 Gарв
 702
 34;
 -----SDGANNETYGFHVDGA
 GGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGA
 monas gingivalis; PG; periodontal disease; gingivitis; antigenic.
 Patterson MA;
 Length 340;
 Antigenic Porphorymonas gingivalis peptides for preventing
 Indels
 .69
 5.2%; Score 195; DB 22;
27.1%; Pred. No. 6.6e-09;
ative 26; Mismatches 69;
 Margetts MB,
 Porphorymonas gingivalis protein PG35.
 Claim 1; Page 474-475; 588pp; English.
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Ж
 AAY34494 standard; Protein; 833
 Hocking DN
Webb EA;
 97AU-0000839.
97AU-0001182.
98AU-0001546.
 172 GAGARYI-----GSMHKG----
 98AU-0002911.
98AU-0003128.
 98WO-AU01023
 98AU-0005028
 98AU-0002264.
 98AU-0003338
 98AU-0003654
98AU-0004917
 Conservative
 (first entry)
 Porphorymonas gingivalis
 Barr IG,
Rothel LJ,
 WPI; 1999-385613/32
 Local Similarity
hes 48; Conserv
 340 AA;
 N-PSDB; AAX91712
 (CSLC-) CSL LTD.
 Porphorymonas
 409929870-A1
 10-DEC-1998;
 22-MAY-1998;
29-JUL-1998;
 25-AUG-1999
 17-JUN-1999
 04-AUG-1998
 10-DEC-1997
 10-JAN-1998
 10-MAR-1998
 09-APR-1998
 23-APR-1998
 05-MAY-1998
 gingivitis
 Agius CT,
 AAY34494;
 Sequence
 vaccine;
 ROBB BC,
 Query Match
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RESULT 45
AAY34368
ID AAY34
XX
AC AAY34
XZ
DT 25-AU
XX
XX
DE Porph
XX
KW Porph
KW vacci
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 Matches 142;
 Query Match
 Sequence
 especially gingivitis.
 activity with a vaccine mechanism of action. The PG polypeptides can used as vaccines especially against Porphorymonas gingivals. Probes be used to detect Porphorymonas gingivals in standard hybridisation assays. Porphorymonas gingivals is involved in periodontal disease
 AAY34368 standard;
 Porphorymonas gingivalis protein PG35
 25-AUG-1999
vaccine; antigenic
 Porphorymonas gingivalis; PG;
 322
 280
 628
 516
 483
 459
 429
 419
 369
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 GFSGGKDFFSLYASAQDVQRRSYYGGGDYTENLLNGAVQSGSTESDEYNDAFTALTSYGT
 GAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGG 310
 QMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTK--AFQGHAAAGFG 190
 NLSQGLKFQPGLRVEDNCQNCGFNQVRINGLEGAYSQILIDSHPIFSSLAGVYGLEQMPA
 EKVHIEKGGSRHVDLYLTEEILSLDGVVVS-ANRNETFRRQAPSLVTVLSPELFLKTNST 146
 TIYNDKDG----VSKVYGVNLEGRIAYNKSFDLQLGG
 TASNSRDDGIFLLMPKHSANL--WTTYQVTPELTIGG 647
 SPNLKEERSRSISASFDYYHRADEWQFNIMGEAFSTFISNQFKPSDKVETTSDGKEWIIR
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 PQTNLDADGKLLKPRQGNQFEVGYK-----GSYMDDRLNARVSFYRMKDKNAAAP----L
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 SYSRP---FRIGHTANE----FVIGADY--NRFRSTNEQGRTTL--YARGGLALNEFRS
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 YGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDA 370
 GV-MVFGQHNYRPGQDIDGDNFTELPNLRNRSL----
 HAKGW-----GSFQNTTQFNGSMLTE---------DRKA
 NM------IERVEVIRGGGSALFGSNAVGGVINVITKEPLRNSAEISHSTMTFD 254
 TFDQLARKTPGLRVLSN--DDGRSSVYARGYE--YSE-------YNIDGLPA 132
 833 AA;
 Conservative
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 --QGGGMYRHTFG-ENWDFTGGLEYIYGQLDDRSGYRPSKIDQNTSTFSQY
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 Protein; 876
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 5.1%; Score 193.5; DB 20;
20.4%; Pred. No. 3.7e-08;
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 periodontal
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 disease; gingivitis;
 660
 -----GFRSYYKTGL 321
 Indels 207;
 Length
 833;
 -STFHPA
 Gaps
 515
 612
 482
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 428
 418
 206
 91
 627
 567
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 368
 279
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 Matches 142;
 Query Match
Best Local
 AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAX94318 to AAX94583. AAX91802 to AAX91898 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation
 Sequence
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 04-AUG-1998;
 10-DEC-1998;
 17-JUN-1999
 Porphorymonas
 especially gingivitis.
 assays. Porphorymonas gingivalis is involved in periodontal disease
 Antigenic Porphorymonas gingivalis peptides
 WPI; 1999-385613/32.
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 09-APR-1998
 10-MAR-1998;
 10-DEC-1997
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 (CSLC-) CSL
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 GV-MVFGQHNYRPGQDIDGDNFTELPNLRNRSI
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 TFDQLARKTPGLRVLSN--DDGRSSVYARGYE--YSE-----YNIDGLPA 132
 EKVHIEKGGSRHVDLYLTEEILSLDGVVVS-ANRNETFRRQAPSLVTVLSPELFLKTNST 189
YSKATLEYHSM---QEYRRGGDRLD---
 YGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDA
 Ġ,
 Similarity
 Page
 Barr IG,
Rothel LJ,
 876 AA;
 LID
 Conservative
 330-331;
 gingivalis.
 98AU-0003128.
98AU-0003338.
98AU-0003654.
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 -NPPFEAQIAEYLOHYINGGSFKFDQ
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 266;
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 Database
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Maximum Match 100%
Listing first 45 summaries
 Total number of hits satisfying chosen parameters:
 Searched:
 Perfect score:
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 Pred. No.
 Score
 d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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US-08-817-707-2
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 US-08-765-081-5

US-09-098-082-5

PCT-US95-06994-5

PCT-US95-06994-8

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US-08-765-081-7
US-09-098-082-7
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|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------|---------|-------|------------------|------------------|-------------------|-------|-------------------|-------------------|-----------------|------------------|------------------|-----|------------------|-------------------|------------------|------|------|
| 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 915 2 US-08-474-373-96 Sequence 915 3 US-08-478-373-96 Sequence 915 3 US-08-478-373-96 Sequence 915 4 US-08-6897-438-96 Sequence 915 4 US-08-6897-438-96 Sequence 915 4 US-08-637-654-96 Sequence 915 4 US-08-637-654-96 Sequence 915 4 US-08-637-18-96 Sequence 916 4 US-08-613-078-96 Sequence 917 4 US-08-613-078-18-96 Sequence 918 3 US-08-613-009A-16 Sequence 918 3 US-08-613-009A-16 Sequence 918 4 US-08-613-009A-16 Sequence 918 4 US-08-487-890A-94 Sequence 918 1 US-08-487-890A-94 Sequence 918 2 US-08-478-373-94 Sequence 918 2 US-08-478-373-94 Sequence 918 3 US-08-478-373-94 Sequence 918 3 US-08-478-371-94 Sequence 918 3 US-08-478-371-94 Sequence | 167.5             | 167.5   | 167.5 | 167.5            | 167.5            | 167.5             | 169.5 | 169.5             | 169.5             | 169.5           | 171              | 172              | 172 | 172              | 172               | 172              | 172  | 7/1  |
| 2 2 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 2 US-08-33/-483-96 Sequence 2 US-08-478-373-96 Sequence 3 US-08-478-373-96 Sequence 3 US-08-478-373-96 Sequence 4 US-08-897-438-96 Sequence 4 US-08-637-654-96 Sequence 4 US-08-637-654-96 Sequence 6 US-08-636-3124A-4 Sequence 7 US-08-817-707-8 Sequence 8 US-08-817-707-8 Sequence 9 US-08-817-908-22 Sequence 9 US-08-478-35-94 Sequence 1 US-08-478-373-94 Sequence 2 US-08-478-373-94 Sequence 3 US-08-478-373-94 Sequence 1 US-08-478-373-94 Sequence 2 US-08-478-373-94 Sequence 3 US-08-478-373-94 Sequence                                    | 4.4               | 4.4     | 4.4   | 4.4              | 4.4              | 4.4               | 4.5   | 4.5               | 4.5               | 4.5             | 4.5              | 4.6              | 4.6 | 4.6              | 4.6               | 4.6              | 4.6  | 4.0  |
| 2 US-08-33-7-93-96 2 US-08-474-671-96 3 US-08-483-577A-96 4 US-08-897-438-96 4 US-08-637-654-96 4 US-08-637-654-96 2 US-08-63-124A-4 4 US-08-63-124A-4 4 US-08-817-707-8 2 US-08-817-707-8 4 US-08-817-708-22 4 US-08-613-09A-16 3 US-08-478-43-94 2 US-08-337-483-94 3 US-08-478-373-94 3 US-08-478-373-94 3 US-08-478-373-94                                                                                                                                                                                                                                                                                                     | -08-478-373-96 Sequence -08-478-373-96 Sequence -08-478-373-96 Sequence -08-483-577A-96 Sequence -08-687-438-96 Sequence -08-637-654-96 Sequence -08-637-654-96 Sequence -08-63-124A-4 Sequence -08-63-124A-4 Sequence -08-817-707-8 Sequence -08-817-707-8 Sequence -08-487-890A-94 Sequence -08-487-890A-94 Sequence -08-478-373-94 Sequence -08-478-373-94 Sequence -08-474-671-94 Sequence -08-474-671-94 Sequence -08-483-577A-94 Sequence                                                                                                                                                                                                                          | 908               | 908     | 908   | 908              | 908              | 908               | 908   | 908               | 908               | 790             | 909              | 915              | 915 | 915              | 915               | 915              | 915  | CTA  |
| US-08-473-373-96 US-08-473-373-96 US-08-483-577A-96 US-08-97-438-96 US-08-637-654-96 US-08-637-124A-4 US-08-637-124A-4 US-08-617-707-8 US-08-613-009A-16 US-08-613-009A-16 US-08-478-35-94 US-08-478-35-94 US-08-478-373-94 US-08-478-373-94 US-08-478-373-94 US-08-478-373-94 US-08-478-571A-94                                                                                                                                                                                                                                                                                                                                   | -08-478-373-96 Sequence -08-478-373-96 Sequence -08-478-373-96 Sequence -08-483-577A-96 Sequence -08-687-438-96 Sequence -08-637-654-96 Sequence -08-637-654-96 Sequence -08-63-124A-4 Sequence -08-63-124A-4 Sequence -08-817-707-8 Sequence -08-817-707-8 Sequence -08-487-890A-94 Sequence -08-487-890A-94 Sequence -08-478-373-94 Sequence -08-478-373-94 Sequence -08-474-671-94 Sequence -08-474-671-94 Sequence -08-483-577A-94 Sequence                                                                                                                                                                                                                          | ω                 | w       | N     | N                | N                | ۲                 | 4     | 4                 | ω                 | 4               | N                | 4.               | 4   | 4                | ω                 | ω                | N    | ٨    |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | US-08-483-577A-94 | -08-474 |       | US-08-337-483-94 | US-08-478-435-94 | US-08-487-890A-94 |       | US-08-778-570B-22 | US-08-613-009A-16 | US-08-817-707-8 | US-08-363-124A-4 | US-08-649-518-96 |     | US-08-897-438-96 | US-08-483-577A-96 | US-08-474-671-96 |      |      |
| <b>D</b> D                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | App]              | ίpp1    | )pp1  | [ppl             | ppl              | [dd               | lgg1  | \pp1              | [dď               | ĭlq             | )pli             | App1             | pp1 | pp1              | [dď               | [gq              | [ppl | Taga |

## ALIGNMENTS

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RESULT 1
US-08-765-081-5
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 APPLICATION NUMBER: US/08/765,081
FILING DATE: March 26, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06994
FILING DATE: June 7, 1995
APPLICATION NUMBER: US 08/265,714
FILING DATE: June 24, 1994
FILING DATE: June 24, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCS/DOCKET NUMBER: CHOR-1-1028
REFERENCS/DOCKET NUMBER: 05,997
REFERENCS/DOCKET NUMBER: 06,997
REFERENCS/DOCKET NUMBER: 07,997
REFERENCS/DOCKET NUMBER: 07,997
REFERENCS/DOCKET NUMBER: 07,997
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
 US-08-765-081-5
 Query Match
Best Local Similarity
Matches 176; Conserv
 Sequence 5, Application US/08765081
Patent No. 5798260
GENERAL INFORMATION:
 ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb
 COMPUTER: IBM PC compatible/Pentium OPERATING SYSTEM: MS-Window 3.1 SOFTWARE: Word for Windows-6.0 CURRENT APPLICATION DATA:
 TOPOLOGY: linear MOLECULE TYPE: protein
 APPLICANT: Tarr, P.I., Bilge, S.S., Besser, T.E., Vary Jr., J.C. TITLE OF INVENTION: Escherichia Coli 0157:H7 Epithelial Adhesin NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 COUNTRY: USA
 STREET: 2800 I
 LENGTH:
 ADDRESSEE:
 RINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPA 68
RITTLASVVIPCLGFS--ASSIAAAEDVMIVSASGY----EK------
 amino acid
OGY: linear
 Washington
 696 amino acids
 3: Christensen, O'Connor, Johnson and Kindne, 2800 Pacific First Center, 1420 Fifth Avenue
 Conservative 103;
 1-206-682-8100; 1-206-224-0718 (direct)
 7.9%; Score 296.5;
21.3%; Pred. No. 1.1e
ative 103; Mismatches
 PCT/US95/06994
 CHOR-1-10286
 .1e-18;
 DB 1;
 304;
 Kindness
 Indels 243;
 Length 696;
 Gaps
 39;
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 Sequence 5, Application US/09098082
Patent No. 6040421
GENERAL INFORMATION
APPLICANT: Tarr, P.I., Bilge, S.S., Besser, T.E., Vary Jr., J.C.
TITLE OF INVENTION: Escherichia Coli 0157:H7 Epithelial Adhesin
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
 ---YARVGGANT-FNIPGSERTWTANLRYSF 722
 ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage
COMPUTER: IBM PC compatible/Pentium II
OPERATING SYSTEM: MS-Windows 95
 CITY: Seattle
STATE: Washington
COUNTRY: USA
 125 YNIDGL----
 276 YDRTLRY---
 348 TPL---
 US-09-098-082-5
 175
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98 ILIDGVRQGGSSDVTPNGFSAMNTGFMPPLAAIERIEVIRGPMSTLYGSDAMGGVVNIIT 157
 216 MAQTVGAS-PRPAEKNNRHETFYAAADW----DI-----NPDTVLGA---G 253
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 Length 696;
 TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
TELEFAX: 1-206-224-0779
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 696 amino acids
TYPE: amino acid
 Query Match 7.9%; Score 296.5; DB 3; Best Local Similarity 21.3%; Pred. No. 1.1e-18; Matches 176; Conservative 103; Mismatches 304;
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/765,081
FILING DATE: March 26, 1997
APPLICATION NUMBER: PCT/US95/06994
FILING DATE: June 7, 1995
APPLICATION NUMBER: US 08/265,714
FILING DATE: June 24, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Sheines, Diana K.
REGISTRATION NUMBER: GAGS TO TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,082
FILING DATE:
Word for Windows-6.0
 , MOLECULE TYPE: protein US-09-098-082-5
 348 TPL-----
 linear
 TOPOLOGY:
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 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-06994-5
 Sequence 5, Application PC/TUS9506994 GENERAL INFORMATION:
 Query Match
Best Local Similarity
 Matches 176;
 TELEFAX: (206) 224 0779
INFORMATION FOR SEQ ID NO: 5:
 APPLICANT:
APPLICANT:
 SEQUENCE CHARACTERISTICS:
LENGTH: 696 amino acids
 NAME: BRODERICK, THOMAS F
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: CHOR-18591
TELECOMMUNICATION INFORMATION:
 FILING DATE: 24-JUN-1994
ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US OF FILING DATE: 24-JUN-1994
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 APPLICANT: BILGE, SIMA S
APPLICANT: BESSER, THOMAS E
APPLICANT: VARY JR, JAMES C
TITLE OF INVENTION: ESCHERICHIA COLI 0157:H7 EPITHELIAL ADHESIN
NUMBER OF SEQUENCES: 14
 APPLICANT:
 CORRESPONDENCE ADDRESS:
 STREET: UC
STREET: SEATTLE
 653
 650
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 596
 38
 69
 APPLICATION NUMBER: PCT/US95/06994 FILING DATE: 07-JUN-95 CLASSIFICATION:
 COUNTRY: USA
ZIP: WA 98101
 TELEPHONE:
 ADDRESSEE:
 N
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 amino acid
 WASHINGTON
 E: CHRISTENSEN, O'CONNOR, JOHNSON AND KINDNESSPLLC
SUITE 2800, 1420 FIFTH AVENUE
 Children's Hospital & Medical Center
University of Washington
Washington State University Research Foundation
TARR, PHILLIP I
 Conservative
 (206)
 Floppy disk
 682 8100
 7.9%; Score 296.5; DB 5 21.3%; Pred. No. 1.1e-18; tive 103; Mismatches 304
 --YARVGGANT-FNIPGSERTWTANLRYSF 722
 -- ASSIAAAEDVMIVSASGY---
 US 08/265,714
 DB 5;
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 Length
 Indels
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 243;
 Gaps
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 PCT-US95-06994-8
 RESULT 4
 Sequence 8, Application PC/TUS9506994
GENERAL INFORMATION:
APPLICANT: Children's Hospital & I
APPLICANT: University of Washingto
 APPLICANT:
APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
 APPLICANT: BILGE, SIMA S
APPLICANT: BESSER, THOMAS E
APPLICANT: VARY JR, JAMES C
TITLE OF INVENTION: ESCHERICHIA COLI 0157:H7
 CORRESPONDENCE ADDRESS
 NUMBER OF SEQUENCES:
 STATE: WASHING
COUNTRY: USA
ZIP: WA 98101
 653
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 SEATTLE 2800,
 WASHINGTON
 Children's Hospital & Medical Center University of Washington
 Washington State University Research TARR, PHILLIP I
 CHRISTENSEN, O'CONNOR,
 -----ERNKISAGYDHTFTFGTWKSY-LNWNET-----ENKGREL
 -RSVLKRDKWGL --- AGQP -
 -----YARVGGANT-FNIPGSERTWTANLRYSF 722
 1420 FIFTH AVENUE
 JOHNSON AND
 EPITHELIAL ADHESIN
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 KINDNESSPLLC
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Best Local Similarity
 RESULT 5
US-09-668-113A-8
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US-09-668-113A-8
 Query Match
 FEATURE:
 477
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 220 VTSLSDTAGTRIPYPTESQNYN--LGARLDWKASEQDVL------256
 SLTG------Y 308
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 9 RINMTAATVLAAL---SSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTK 65
 ---KLTNAAASVSVISQEELQSSQYHDLAEALRSVEGVDVESGTGKTGGLEISIRGMPAS
 172 LVRKRPTKAFQGHAAAG-----FGTHKQYK-----AEADVSGSLNSDGSVRGR----
 160 IITRKNADKWLSSVNAGLNLQESNKWGNSSQFNFWSSGPLVDDSVSLQVRGSTQQRQGSS
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 Query Match 7.6%; Score 286; DB 5; Length 703; Best Local Similarity 20.4%; Pred. No. 1.1e-17; Matches 171; Conservative 104; Mismatches 304; Indels 258;
 protein
E. coli O157:H7 adhesin amino acid sequence,
wherein "Xaa" residues represent gaps
introduced to facilitate best alignment with
SEQ ID NO:9.
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06994
FILING DATE: O'-JUN-95
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 080/265,714
FILING DATE: 24-JUN-1994
ATTORNEY/AGRIT INFORMATION:
NAME: BRODERICK, THOMAS F
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: CHOR-18591
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (206) 622 8100
TELEPRAX: (206) 224 0779
INPORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acids
TYPE: amino acids
 ORGANISM: Escherichia coli O157:H7
STRAIN: 86-24 NALR
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 TOPOLOGY: lin
MOLECULE TYPE:
DESCRIPTION:
DESCRIPTION:
DESCRIPTION:
 ORIGINAL SOURCE
 DESCRIPTION:
 HYPOTHETICAL
 PCT-US95-06994-8
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 GVETEISGAVTPKWQ----IHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQVT 640
 ----FSPRAYLVWDVADAWTLKGGVTTGYKAPRMGQLHKGISGVSGQGKTNLLGNPDL 476
 641 PELTIGGGV------NAMSGITSSA----GMHAGGYATFDAMAAYRFTPKLKL 683
 |: | | ::: | | | EEVASWIGARYRGKTPRFTQNYSSLSAVQKKVYDEKGEYLKAWTVVDAGLSWKMTDALTL 648
 65 KIPASLREIPQSVSIITNQQVKDR-NVDTFDQLARKTPGLRVLSN-----DDGRSSVY 116
 | | : |||:|| :| GMGPENTLILIDGVPVTSRNSVYSWRGERDTRGDTNRWVPP-EQVERIEVIRGPAAARYG 157
 SGAAGGVVNIITKRPTNDW--HGSLSLYTNQPESSEEGATRRANFSLSGPLAGDALTTRL 215
 212 RGRV------MAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLG--AGYLYQQRH 260
 ----NIYAGDIQNSSSAVTESLAKSGKETNRLYRQNYGI----TH----NGIWDWGOSRF 322
 117 ARGYEYSEYNIDGLPAQMQS-----INGTLPNLFAFDRVEVMRGPSGLFDS 162
 SGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEA-----DVSGSLNSDG---SV 211
 216 YGNLNKTDADSWDINSPVGTKNAAGHEGVRNKDINGVVSWKLNPQQILDFEVGYSRQG-- 273
 LAPYNGLPADANNKLPSLPQHVFV--GADWNKFKMNSHDVFADLKHYFGNG----GYGKV 314
 GMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSR 374
 GVYYEKTN-----FITNRINEGLSGGGEGRILLAGEK-------FTTNRLS 358
 375 PFRLGNTAN------EFVIGADYNRFRSTNEOGRTTLYARGGLALNEFRSIPQVDLI 425
 5 MSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTERNGDYSSFAVTVGT 64
 649 NAAVNNLLNKDYSDVSLYSAGKSTLYAGDYFQTGSSTTGYVIP--ERNYMMSLNYQF 703
 KPEESVSYEAGV---YYDNPAGLNANVTGFMTDFSNKIXVSYSINDNTNSYVNSGKARLH
 684 QINADNIFNRHY-------YARVGGANT-FNIPGSERTWTANLRYSF 722
 KPROGNOFEVGYKGSYMDD--RLNARVSFYRMKDKN-AAAPLNPNNKKTRYAALGKRVME
 GENERAL INFORMATION:
APPLICANT: Russo, Thomas A.
TITLE OF INVENTION: Identification of A Vaccine Candidate from an
TITLE OF INVENTION: Extraintestinal Strain of E. coli
FILE REFERENCE: 11520.0214
 Indels 247;
 Length 725;
 7.2%; Score 273.5; DB 4;
19.8%; Pred. No. 1.7e-16;
 Matches 167; Conservative 127; Mismatches 304;
 CURRENT APPLICATION NUMBER: US/09/668,113A
CURRENT FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 8
LENGTH: 725
 // Sequence 8, Application US/09668113A
// Patent No. 6410703
 TYPE: PRT
ORGANISM: Escherichia coli
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 PCT-US95-06994-6
 Sequence 6, Application:
Sequence 6, Application:
GENERAL INFORMATION:
APPLICANT: Children's Hospital & Medical Center
APPLICANT: University of Washington
APPLICANT: Washington State University Research
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/265,714
FILING DATE: 24-UN-194
ATTORNEY/AGENT INFORMATION:
NAME: BRODERICK, THOMAS F
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: CHOR-18591
TELECOMMUNICATION INFORMATION:
 TELEFAX: (206) 224 0779 INFORMATION FOR SEQ ID NO: 6:
 APPLICANT:
APPLICANT:
APPLICANT:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06994
FILING DATE: 07-JUN-95
 NUMBER OF SEQUENCE:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTENSEN, O'CONNOR, JOHN
ADDRESSEE: 2800, 1420 FIFTH AVENUE
 SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acid
 APPLICANT: BESSER, THOMAS E
APPLICANT: VARY JR, JAMES C
TITLE OF INVENTION: ESCHERICHIA COLI 0157:H7 EPITHELIAL
NUMBER OF SEQUENCES: 14
 664
 614
 561
 573
 513
 721
 718
 623
 461
 469
 405
 426
 TELEPHONE:
 VTASE
 PLSVIPKYTINNSLNWTITQAFSASFNWTLYGRQKPRTHAETRSEDT---GGL------
 LYTPOTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKK 572
 LRYSF 722
 -SGKELGAYSLVGTNFNYDINKNLRLNVGVSNILNKQIFRSSEGANTYNEPG--RAYYAG
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 FL-LMPKHSAN-
 TASGAYILKWQNGGKALVDGIEASMSFPLVKERLNWNTNATW-----MITSEQKDTGN
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 ----LGHY-KIESGEGKT-----LHKASKTKFTGYA-----GAVYDLNDNNSLYLSLSQ
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 ----SGISGSAADRSSKNHSQISALYIEDNIEPVPGTNIIPGLRFDYLSDSGGNFSPSLN
 WA 98101
amino acid
 WASHINGTON
 718 amino acids
 BILGE, SIMA S
 (206)
 682 8100
 CHOR-18591
 --LWTTY-----QVTPELTIGGGVNAMSGITS
 JOHNSON
 #1.30
 AND
 KINDNESSPLLC
 Foundation
 ADHESIN
 613
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 512
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 PCT-US95-06994-6
 Matches 156;
 Query Match
Best Local Similarity
 TOPOLOGY: lin
MOLECULE TYPE:
DESCRIPTION:
DESCRIPTION:
 ORIGINAL SOURCE:
 HYPOTHETICAL:
 340
 607
 549
 588
 492
 537
 432
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 280
 235
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 175
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 687 ADNIFNRHY----
 55
 76 SYSIITNQQVKDRNVDTFDQLARKTPGLRVLS--NDDGRSSVYARGY--EYSEYNIDGL- 130
 ORGANISM: Escherichia coli O157:H7 STRAIN: 86-24 NALR
 DESCRIPTION:
DESCRIPTION:
 VVLASTGETFRQKSWSVFAEDEWHLTDALALTAGSRYEHHEQFGGH---
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| SVSVISQEELQSSQYHDLAEALRSVEGVDVESGTGKTGGLEISIRGMPASYTLILIDGVR 114
 ASWLGARYRGKTPRFTQNYSSLSAVQKKVYDEKGEYLKAWTVVDAGLSWKWTDALTLNAA
 GXXXXXTLPLWSEDVTLSLNYTWTRSEQRDGDNK--GAPLSYTPEHMVNAKLNWQITEEV
 AGV---YYDNPAGLNANVTGFMTDFSNKIXXVSYSINDNTNSYVNSGKAXXXRLHGVEFA
 RAYLVWDVADAWTLKGGVTTGYKAPRMGQLHKGISGVSGQGKTNLLGNPDLKPEESVSYE
 YAGAVYDLNDNNSL-----YLS--LSQLYTPQTNLDADGKL------LKPRQGNQFE
 KGRELVRSVLKRDKWGLA-GQPRELKESNLILNSLLLTPLGESHLVTVGGEFQSSSMKDG
 AGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNE
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 GAS-PRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLP
 QGHAAAG-----VMAQTV 220
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VNNLLNKDYSDVSLYSAGKSTLYAGDYFQTGSSTTGYVIP--ERNYWMSLNYQF
 TEISGAVTPKWQ----IHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQVTPEL
 VGYKGSYMDD--RLNARVSFYR--MKDKNAAAPLNPNNKKTRYAALGKRV---MEGVE--
 QGRTTLYA-----RGGLALNEFRSIPQVDLIANA-RKGVRGYSHTVA-------
 GTRIPYPTESQNYN--LGARLDWKASEQDVL---
 LSSVNÄGLNIQESNKWGNSSQFNFWSSGPLVDDSVSLQVRGSTQQRQGSSVXXTSLSDTA
 -----TENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTG
 Conservative
 -W--FDMDT-----LGSLTG----
 linear
 NO
 protein
E. coli 0157:H7 adhesin amino acid sequence, wherein "Xaa" residues represent gaps
 introduced to facilitate SEQ ID NO:7.
 7.0%;
 -GYDRTLRYERNKISÁGYDGTFTFGTWKS-----YLNWNETEN
 -NAMSGITSSA----GMHAGGYATFDAMAAYRFTPKLKLQIN
 ----YARVGGANT-FNIPGSERTWTANLRYSF 722
 99;
 Score 264.5; DE
Pred. No. 1.1e-1
9; Mismatches 2
 best alignment with
 DB 5;
 282;
 Indels 237;
 Length 718;
 -----FSP
 Gaps
 686
 643
 548
 431
 492
 382
 440
 323
 339
 279
 234
 174
 999
 909
 587
 491
 536
 399
 286
 263
 35;
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RESULT 7 US-08-765-081-7 ; Sequence 7, Application US/08765081 ; Patent No. 5798260 9

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684 QINADNI 690
 RAGVLNL 626
 FILING DATE:
 TOPOLOGY:
 COUNTRY:
 US-09-098-082-7
 268
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 36;
 FRLGNTANEFV-IGADY-----NRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLI 425
 60 VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG 119
 120 YE--YSEYNIDGLPAQMQSINGTLPN-----LFAFDRVEVMRGPSGLFDSSGEMGG 168
 94 LDSSYTLILVDG--KRVNSRNAVFRHNDFDLNWIPVDSIERIEVVRGFMSSLYGSDALGG 151
 169 IVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAE 228
 152 VVNIITKKIGQKW-----E 176
 284 VGADWN-KFKM---NSHDVFADLKHYFGNGGYGKVGMRYSDRDADS-----NYA-- 328
 ------FAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRP 375
 281 HNGRWDYGTSELKYYGEKVENKNP------GNSSPITSESNTVDGKYTLP 324
 229 KNNRHETFYAAADWDINP--DTVLGA---GYLYQQRHLAPYNGLPADANNKLPSLPQHVF 283
 Gaps
 APPLICANT: Tarr, P.I., Bilge, S.S., Besser, T.E., Vary Jr., J.C. TITLE OF INVENTION: Escherichia Coli 0157:H7 Epithelial Adhesin NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
 Query Match 6.9%; Score 260; DB 1; Length 663; Best Local Similarity 20.8%; Pred. No. 2.6e-15; Matches 151; Conservative 106; Mismatches 240; Indels 230;
 E: Christensen, O'Connor, Johnson and Kindness 2800 Pacific First Center, 1420 Fifth Avenue
 MOLECULE TYPE: protein DESCRIPTION: E. coli CirA protein amino acid sequence
 TELEPHONE: 1-206-682-8100; 1-206-224-0718 (direct) TELEFAX: 1-206-224-0779 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
 COMPUTER: IBM PC compatible/Pentium
OPERATING SYSTEM: MS-Window 3.1
SOFTWARE: Word for Windows 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,081
FILING DATE: March 26, 1997
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06994
FILING DATE: June 7, 1995
APPLICATION NUMBER: US/08/565,714
FILING DATE: June 7, 1995
APPLICATION NUMBER: US/08/265,714
FILING DATE: June 7, 1994
ATORNEY AGENT INFORMATION:
NAME: Shelton, Dennis K.
REFERENCE/DOCKET NUMBER: CHOR-1-10286
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 ORGANISM: Escherichia Coli
 LENGTH: 663 amino acids
TYPE: amino acid
 ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 CITY: Seattle
STATE: Washington
COUNTRY: USA
GENERAL INFORMATION:
 HYPOTHETICAL: DORIGINAL SOURCE:
 TOPOLOGY:
 US-08-765-081-7
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325 L---TAINQFLTVGGEWRHDKLSDAVNLTGGTSSKTSASQYAL--FVEDEWRIFEPLALT 379 426 ANARKGVRGYSHTVATENLDEFGIYGKS-----TFHPADGLSLIGGGRLGHYKIESGE 478 532 GNQFEVG--YKGS------YMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYA 576 ----MEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFL 624 625 LMPKHSA-NLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKL 683 479 GKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKL-----LKPRQ 531 414 WATAFKAP----------SLLQLSPDWTSNSCRGACKIVGSPDLKPET 451 Sequence 7, Application US/09098082

Patent No. 6040421

GENERAL INFORMATION:
APPLICANT: Tarr, P. I., Bilge, S.S., Besser, T.E., Vary Jr., J.C.
TITLE OF INVENTION: Escherichia Coli 0157:H7 Epithelial Adhesin
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue MOLECULE TYPE: protein DESCRIPTION: E. coli CirA protein amino acid sequence HYPOTHETICAL: NO ORIGINAL SOUNES: NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: CHOR-1-12402
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
TELEPRAX: 1-206-224-0779
INFORMATION FOR SEQ ID NO: 7: Diskette-3.5 inch, 1.44Mb storage COMPUTER: IBM PC compatible/Pentium II OPERATING SYSTEM: MS-Windows 95 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/765,081
FILING DATE: March 26, 1997
APPLICATION NUMBER: PCT/US95/06994
FILING DATE: June 7, 1995
APPLICATION NUMBER: US 08/265,714
FILING DATE: June 24, 1994
ATTORNEY/AGENT INFORMATION: OPERATING SYSTEM: MS-Windows 95 SOCTWARE: WORD FOR WINDOWS-6.0 SUCREBUT APPLICATION DATA: APPLICATION NUMBER: US/09/098,082 663 amino acids SEQUENCE CHARACTERISTICS: LENGTH: 663 amino acid ZIP: 98101-2347 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette Washington TYPE: amino acid linear 577 ALGKRV-----

CORRESPONDENCE ADDRESS:

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RESULT 9
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) ORGANISM:
US-09-098-082-7
 Sequence 9, Applicati
GENERAL INFORMATION:
 Matches
 Query Match
 APPLICANT:
APPLICANT:
TITLE OF IN
 APPLICANT:
 APPLICANT:
APPLICANT:
 APPLICANT:
 510
 452
 414
 169
 620
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 568
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 479
 380
 426
 325
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 281
 329
 284
 177
 120
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 229
 152 VVNIITKKIGQKW-----
 94
 34
 Local Similarity
 60 VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG 119
 LDSSYTLILVDG--KRVNSRNAVFRHNDFDLNWIPVDSIERIEVVRGPMSSLYGSDALGG
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 VVTASSVEQNÍKDAPASISVÍTQEDLQRKPVQNLKDVLKEVPGVQLTNEGDNRKGVSIRG
 RAGVLNL
 QINADNI 690
 ANGRRIPVFSYYNVNKARNQGVETELKIPFNDEWKLSINYTY--NDGRDVSNGENKPLSD
 SESWELGLYYMGEEGWLEGVESSVTVFRND-VKDRISISRTSDVN-AAPGYQNFVGFETG
 GNOFEVG--YKGS------YMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYA
 GKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKL-----LKPRQ 531
 VGADWN-KFKM---NSHDVFADLKHYFGNGGYGKVGMRYSDRDADS-----NYA-- 328
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 L-PFHLALEDWSFY--
 LMPKHSA-NLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKL 683
 ALGKRV------MEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFL
 ANARKGVRGYSHTVATENLDEFGIYGKS-----TFHPADGLSLIGGGRLGHYKIESGE 478
 L---TAINQFLTVGGEWRHDKLSDAVNLTGGTSSKTSASQYAL--FVEDEWRIFEPLALT
 FRLGNTANEFV-IGADY------NRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLI 425
 HNGRWDYGTSELKYYGEKVENKNP------GNSSPITSESNTVDGKYTLP
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 HRDRGDT-YNGQFFTSGPLIDGVLGMKAYGSLAKREKDDPQNSTTTD-TGETPRI--EGF
 KNNRHETFYAAADWDINP--DTVLGA---GYLYQQRHLAPYNGLPADANNKLPSLPQHVF
 YE--YSEYNIDGLPAQMQSINGTLPN-----LFAFDRVEVMRGPSGLFDSSGEMGG 168
 -----FAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRP 375
 151;
 ဝှု
 T: Children's Hospital & Medical Center
T: University of Washington
T: Washington State University Research Foundation
T: TARR, PHILLIP I
T: BIAGE, SIMA S
T: BESSER, THOMAS E
T: VARY JR, JAMES C
INVENTION: ESCHERICHIA COLI 0157:H7 EPITHELIAL ADHESIN
 Application PC/TUS9506994
SEQUENCES:
 6.9%; Score 260; DB 3; ilarity 20.8%; Pred. No. 2.6e-15; Conservative 106; Mismatches 240
 626
 Escherichia Coli
 ----MDDHETYGEHWSPRAYLVYNATDTVTVKGG--------
 -----SLLQLSPDWTSNSCRGACKIVGSPDLKPET
 -----E
 - VSGHYTGQKRADSATAKTPGGYTIWNTGAAWQVTKDVKL
 240;
 Length 663;
 Indels
 230;
 Gaps
 619
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 PCT-US95-06994-9
 Query Match 6.2%; Score 232.5; DE Best Local Similarity 20.2%; Pred. No. 1e-12; Matches 151; Conservative 108; Mismatches 2
 TELEFAX: (206) 224 07: INFORMATION FOR SEQ ID NO:
 HYPOTHETICAL: N
ORIGINAL SOURCE:
ORGANISM: ESC
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/265,714
FILING DATE: 24-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BRODERICK, THOMAS F
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: CHOR-18591
 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06994
 TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: E. coli CirA protein amino acid sequence,
DESCRIPTION: wherein "Xaa" residues represent gaps
 SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 682 8100
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 DESCRIPTION: 1HC
DESCRIPTION: SEC
DESCRIPTION: NO
 355
 281
 326
 279
 181
 224
 152
 164 GEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGAS
 118
 ADDRESSEE: CHRISTENSEN,
STREET: SUITE 2800, 1420
CITY: SEATTLE
 94
 60
 34 VVTASSVEQNÍKDAPASISVÍTQEDLQRKPVQNLKDVLKEVPGVQLTNEGDNRKGVXXSI 93
 FILING DATE: 0 CLASSIFICATION:
 COUNTRY: USA
ZIP: WA 98101
 DALGGVVNIITKKIGQKW------SGTVTVDTTIQ-----
 VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA--
 VGLGTEIKOKALAFDASYSRPFRLGNTANEFV-IGADY-----
 PRPAEKNNRHETFYAAADWDINP--DTVLGA---GYLYQQRHLAPYNGLPADANNKLPSL
 RGLDSSYTLILVDG--KRVNSRNAVFRHNDFDLNWIXXXPVDSIERIEVVRGPMSSLYGS
 RGYE--YSEYNIDGLPAQMQSINGTLPN-----LFAFDRVEVMRGPSGLFDSS 163
PGNSSPITSESNTVDGKYTLPL---TAINQFLTVGGEWRHDKLSDAVNLTGGTSSKTSAS
 PQHVFVGADWN-KFKM---NSHDVFADLKHYFGNGGYGKVGMRYSDRDADS-----
 ----EHRDRGDT-YNGQFFTSGPLIDGVLGMKAYGSLAKREKDDPQNSTTTD-TGETPRI
 --EGFSSRDGNVEFAWTPNONHDFTA------GY---GFDRODRDSDSLDKNXXXXX
 amino acid
 -----NYAFAGSKLGMKTPAGRPGCNTADDK-----
 WASHINGTON
 ESCHERICHIA COLI
 Floppy disk
 introduced to facilitate best alignment with SEQ ID NO:8.
 07-JUN-95
 ± 0779

± 0779

• 9:
 1420
 O'CONNOR, JOHNSON AND KINDNESSPLLC
O FIFTH AVENUE
 GRWDYGTSELKYYGEKVENKNXXXXXXXXXXXXXX 332
 DB 5;
 246;
 #1.30
 Indels 243;
 Length
 -NRFRSTNEQGRTT 404
 703;
 Gaps
 325
 234
 223
 354
 278
 180
 151
 117
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32;

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Local Similarity
 Matches 147;
 US-09-098-082-6
 289
 415
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 390 QYAL--FVEDEWRIFEPLALTT----GVR-------MDDHETYGEHWSPRAYLVYNA 433
 458 ADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQ 517
 ----SLLOLSPDW 459
 518 INLDADGKL------YMDDRLNARVSFY 555
 -- MEGVETEISGAVTPKWQIHAG 603
 519 RTSDVN-AAPGYQNFVGFETGANGRRIPVFSYYNVNKARNQGVETELKIPFNDEWKLSIN 577
 YSYLHSQIKTASNSRDDGIFLLMPKHSA-NLWTTYQVTPELTIGGGVNAMSGITSSAGMH 662
 405 LYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKS-----TFHP 457
 578 YTY--NDGRDVSNGENKPLSDL-PFHLALEDWSFY-----VSGHYTGQKRADSATAKT 627
 GENERAL INFORMATION:
APPLICANT: Tarr, P.I., Bilge, S.S., Besser, T.E., Vary Jr., J.C.
TITLE OF INVENTION: Escherichia Coli 0157:H7 Epithelial Adhesin
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
 E: Christensen, O'Connor, Johnson and Kindness 2800 Pacific First Center, 1420 Fifth Avenue
 seguence
 NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: CHOR-1-10286
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0718 (direct)
TELEPAS: 1-206-224-0779
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
 Diskette-3.5 inch, 1.44Mb storage
 MOLECULE TYPE: protein
DESCRIPTION: Vibrio cholerae IrgA amino acid
 APPLICATION NUMBER: US/08/765,081
FILING DATE: March 26, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06994
FILING DATE: June 7, 1995
APPLICATION NUMBER: US 08/265,714
FILING DATE: June 24, 1994
ATTORNEY/AGENT INFORMATION:
 COMPUTER: IBM PC compatible/Pentium
OPERATING SYSTEM: MS-Window 3.1
SOFTMARE: Word for Windows-6.0
CURRENT APPLICATION DATA:
 434 TDTVTVKGG-------WATAFKAP----
 AGGYATFDAMAAYRFTPKLKLQINADNI 690
 | | | :: | | :: | :: | :: | BGGYTIWNTGAAWQVTKDVKLRAGVLNL 655
 RMKDKNAAAPLNPNNKKTRYAALGKRV---
 Sequence 6, Application US/08765081
Patent No. 5798260
 Vibrio Cholerae
 : 652 amino acids
amino acid
 ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 CITY: Seattle
STATE: Washington
COUNTRY: USA
 linear
 ORIGINAL SOURCE
 HYPOTHETICAL:
 ADDRESSEE:
 TOPOLOGY:
 US-08-765-081-6
 LENGTH:
 STREET:
 663
 628
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Length 652;

DB 1;

5.6%; Score 212;

Query Match

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70 TDALKSVPGVTVTGGGDTTDISIRGMGSNYTLILVDGKRQTSRQTRPNSDGPGIEQGWLP 129
 143 NLPAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVS 202
 254 YLYQQRH-----LAPYNGLPADANNKLPSLPQHVFVGADWNKFKMN----SHDVFADLKH 304
 333 MLSFGVEGKHESLE-----DKTSNKI----SRTHISNTQW-----AGFIE 369
 114 NEFRSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHP-----ADGLSLIGG 466
 370 DEWALAEQFRLTFGGR------LDHDKNYG-SHFSPRVYGVWNLDPLWTVKG 414
 467 GRLGHYKIESG-EGKTLHKASKT--KFTGYAGAVY---DLNDNNSLYLSLSQLYTPQTNL 520
 G-----VSTGFRAPQLREVTPDWGQVSG-GGNIYGNPDLQPETSINKELSLMYSTGSGL 467
 521 DADGKLIKPROGNOFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLN----PNN---KK 572
 573 TRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSAN 632
 633 LWTTYQVTPELTIGGGVN-----AMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQIN 686
 305 YFGNGGYGKVG-----MRYSDRDADS-----NYAFAGSKLGMKTPAGRPGCNTADDKAC 353
 354 AVGLGTEIKOKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEOGRTTLYARGGLAL 413
 562 ANLSWQTTDRLNSWANLNYRGKEMQPEGGASNDDFIAPSYTFIDTGVTYALTDTATIKAA 621
ilarity 19.6%; Pred. No. 7.4e-11;
Conservative 99; Mismatches 299; Indels 204; Gaps
 ---LREIPQSVSIITNQQVKDRNVDTF 93
 203 GSLNSDGSVRGRVMAQTVGASPRPAEKNNRH-----ETFYAAADWDINPD--TVLGAG
 468 AAS------LTAFHNDFKDKITRVACPANICTAGPNOMGATP
 APPLICANT: Tark, P.I., Bilge, S.S., Besser, T.E., Vary Jr., J.C.
TITLE OF INVENTION: Escherichia Coli 0157:H7 Epithelial Adhesin
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
CITY: Seartle
STATE: Mashington
 250 VSAQDRENNVGKSAQSSGCRGTCSN-----TD-NOYRRNHVAVSH----
 94 DOLARKTPGLRVLSNDDGRS-SVYARGYEYSEYNIDGLPAQMQSI----
 ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage
 687 ADNIFNRHY-YARVGGANTFNIPGSERTW 714
 622 VYNLFDQEVNYAEYG----YVEDGRRYW 645
 Sequence 6, Application US/09098082
Patent No. 6040421
GENERAL INFORMATION:
 57 SFAVTVGTKIPAS.
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 ; ORGANISM: Vibrio Cholerae US-09-098-082-6
 Query Match
Best Local Similarity
 Matches 147;
 TELEFAX: 1-206-224-0779
INFORMATION FOR SEQ ID NO: 6:
 ORIGINAL SOURCE:
 MOLECULE TYPE: protein DESCRIPTION: Vibrio HYPOTHETICAL: NO
 APPLICATION NUMBER: US 08/765,081
FILING DATE: March 26, 1997
APPLICATION NUMBER: PCT/US95/06994
FILING DATE: June 7, 1995
APPLICATION NUMBER: US 08/265,714
FILING DATE: June 24, 1994
ATTORNEY/AGENT INFORMATION:
 SEQUENCE CHARACTERISTICS:
 TELECOMMUNICATION INFORMATION:
 PRIOR APPLICATION DATA:
 CURRENT APPLICATION DATA:
 305
 521
 414 NEFRSIPOVDLIANARKGVRGYSHTVATENIDEFGIYGKSTFHP-----ADGLSLIGG 466
 254 YLYQQRH-----LAPYNGLPADANNKLPSLPQHVFVGADWNKFKWN----SHDVFADLKH 304
 190
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 130
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 354 AVGLGTEIKOKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEOGRTTLYARGGLAL 413
 COMPUTER: 15"...
OPERATING SYSTEM: MS-Windows-6.0
COMPUTER: Word for Windows-6.0
COMPUTER: YOUR NATA:
 NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: CHOR-1-12402
 70
 94
 10
 57 SFAVTVGTKIPAS------93
 TOPOLOGY:
 TELEPHONE:
 APPLICATION NUMBER:
 ENGTH:
 YFGNGGYGKVG-----MRYSDRDADS-----NYAFAGSKLGMKTPAGRPGCNTADDKAC 353
 GSLNSDGSVRGRVMAQTVGASPRPAEKNNRH-----ETFYAAADWDINPD--TVLGAG 253
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 SLSVTLGLMFSASAFAQDATKTDETMVVTAAGYAQVIQNAPASISVISREDLESRYYRDV 69
DADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLN-----PNN---KK 572
 G-----VSTGFRAPQLREVTPDWGQVSG-GGNIYGNPDLQPETSINKELSLMYSTGSGL
 DEWALAEQFRLTFGGR----
 MLSFGVEGKHESLE-----AGFIE 369
 ---QGDWQGVGQSDTYLQYEENTNKSREMSIDNTVF---KSTLVAPIGEH-----
 VSAQDRENNVGKSAQSSGCRGTCSN-----TD-NQYRRNHVAVSH-----
 ANFFVTGPLSDALSLQVYGQTTQRDEDEIEHGYGDKSLRSLTSKLNYQLNPDHQLQLEAG
 NLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVS
 DQLARKTPGLRVLSNDDGRS-SVYARGYEYSEYNIDGLPAQMQSI-----NGTLP 142
 GRLGHYKIESG-EGKTLHKASKT--KFTGYAGAVY---DLNDNNSLYLSLSQLYTPQTNL 520
 H: 652 amino acids amino acid
 5.6%; Score 212; DB 3; Length 652; ilarity 19.6%; Pred. No. 7.4e-11; Conservative 99; Mismatches 299; Indels 2
 linear
 1-206-682-8100; 1-206-224-0735 (direct)
 IBM PC compatible/Pentium YSTEM: MS-Windows 95
 Vibrio cholerae IrgA amino acid sequence
 US/09/098,082
 -----LDHDKNYG-SHFSPRVYGVWNLDPLWTVKG
 H
 Indels 204;
 Gaps
 332
 249
 189
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 US-08-537-361E-4
 US-08-537-361E-4
 Sequence 4, Application US/08537361E Patent No. 6121037
GENERAL INFORMATION:
 Matches 172;
 Query Match
 TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6121037nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 94,7
TELECOMMUNICATION INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,361E
FILING DATE: 02-OCT-1995
 APPLICANT:
 APPLICANT:
 MOLECULE TYPE:
 CORRESPONDENCE ADDRESS:
 APPLICANT: Nassif, Xavier
TITLE OF INVENTION: No. 6121037el Bacterial Hemoglobin Receptor
TITLE OF INVENTION: Genes and Uses
 NUMBER OF SEQUENCES:
 573
 687 ADNIFNRHY-YARVGGANTFNIPGSERTW 714
 504
 468
118 RGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKR- 176
 622 VYNLFDQEVNYAEYG----YVEDGRRYW 645
 633 LWTTYQVTPELTIGGGVN-----AMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQIN 686
 STREET: 300 St
CITY: Chicago
 61
 65
 10
 TOPOLOGY:
 TELEPHONE:
 14 AATVLAALSSSVFAAQTADLET-----VHIKGQRSYNAIVTEKNGDYSSFAVTVGT 64
 Local Similarity
 TYPE:
 COUNTRY:
 ADDRESSEE:
 LENGTH:
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 TRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSAN
 KIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDG------RSSVYA 117
 AALLGSIFGNPVFAADEAATETTPVKAEVKAVRVKGORNAPAAVER-----VNLNR 60
 ANLSWOTTDRINGWANLNYRGKEMOPEGGASNDDFIAPSYTFIDTGVTYALTDTATIKAA 621
 AAS---
 TYRVNIDEAETYGAEATLSLPITESVELSSSYTYTHSEQKSGNFAGRP--LLQLPKHLFN
 60606
 amino acid
 Illinois
 791 amino acide
 E: McDonnell Boehnen Hulbert
300 South Wacker Drive, 32nd
 USA
 So, Magdalene
 Stojiljkovic,
 Conservative 103;
 Heffron, Fred
 312-913-0001
 protein
 Vivian
 19.4%;
 '4.9%; Score 186.5; DB 3; 19.4%; Pred. No. 2.4e-08;
 14
 -----LTAFHNDFKDKITRVACPANICTAGPNQWGATP
 Igor
 M
 Mismatches 329;
 & Berghoff
Floor
 Length 791;
 Indels 283;
 Gaps
 632
 503
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 588 VKDAQYTVYENKGWGTPLQKKVKDYPWLNKSAY-VFDMYGFYKPAKNLTLRAGVYNLFNR 746
RDLLLPERQFGVMMKNGYSTRNREWTNTLGFGVSNDRVDAALLYSQRRGHETESAGKRGY 227
 KAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYL 255
 228 PVEGAGSGA-NIRGSARG-----IPDPSQ--HKYHSFLGKIAYQINDNHRIGASLN 275
 276 GOOGHNYTVEESYNLLASYWREADDVNRRRNTNLFYEWTPESDRLSMVKADVDYOKTKVS 335
 295 SHDVFADLKHYFGN--GGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKA 352
 ----- 368
 353 CAVGLGTEIKOKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEOGRTTLYARGGLA 412
 -----GRHRLSFKTFAG 399
 413 INEFRSIPQVDLIANAR--KGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLG 470
 ORDFENLINRDDYYFSGRVVRTTNSIOHPVKTTN---YGFSLSDQIOWNDVFSSRAGIRYD 456
 HYKIESGE-GKTLHKASKT-----KFTGYAGAV------YDLNDN----NS 505
 GAVTPKWQIHAGYSYLHSQ------IKTASNSRDDGIFLLMPKHSANL 633
 SFVPEGWKLFGSLGYAKSKLSGDNSLLSTQPLKVIAGIDYESPSEKWGVFSRLTYLGAKK 687
 634 WTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNR 693
 ------HKOY 195
 256 YOORH-----LAPYNGLPADANNK-----LPSLPQHVFVGA--DWNKFKAN 294
 LYLSL---SQLYTPQTNLDADGKL-----LKPR-----QGNQFEVGYKGSYMDDRLNAR 551
 576 VSGTPGCTEEDAYYYRCSD------PYKEKLDWQMKNIDKARIRGIELTGRLNVDKVA 627
 VS------FYRMKDKNAAAPLNPNNKKTRYAA--LGKRVMEGVE-----TEIS
 APPLICANT: Soillikovic, Igor
APPLICANT: Bo, Magdalene
APPLICANT: Hwa, Vivian
APPLICANT: Heffron, Fred
APPLICANT: Nassif, Xavier
APPLICANT: Nossif, Xavier
TITLE OF INVENTION: No. 6277382el Bacterial Hemoglobin Receptor
TITLE OF INVENTION: Genes and Uses
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
 HY------YARVG-----GANTFNIPGSERTWTANLRYSF 722
 747 KYTTWDSLRGLYSYSTTNAVDRDGKGLDRYRAPG--RNYAVSLEWKF 791
 ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive, 32nd Floor CITY: Chicago STATE: Illinois
 ----PIKAF----QGHA-----AAGFGT---
 A-----VNYKGSFPTNYTTWETEYHKKEVGEIY
 -----TTFKRITLRMD---SHPLQLGG-----
 Sequence 4, Application US/08817707 Patent No. 6277382 GENERAL INFORMATION:
 COMPUTER READABLE FORM:
 RESULT 13
US-08-817-707-4
 121
 168
 400
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61 IKQEMIRDNKDLVRYSTDVGLSDRSRHQKGFAIRGVEGDRVGVSIDGVNLPDSEENSLYA 120
 RGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKR- 176
 65 KIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDG-----RSSVYA 117
 121 R---YGNFNSSRLSIDPELVR-----NIDIVKGADSFNTGSGALGGGVNYQTLQG 167
 196 KAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYL 255
 256 YQQRH------LAPYNGLPADANNK------LPSLPQHVFVGA--DWNKFKMN 294
 295 SHDVFADLKHYFGN--GGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKA 352
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 353 CAVGLGTEIKOKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEOGRTTLYARGGLA 412
 369 -----TTFKRITLRMD---SHPLQLGG------------------------------GRHRLSFKTFAG 399
 113 LNEFRSIPQVDLIANAR--KGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLG 470
 400 QRDFENLNRDDYYFSGRVVRTTNSIQHPVKTTN---YGFSLSDQIQWNDVFSSRAGIRYD 456
 HTKMTPQELNADCHACDKTPPAANTYKGWSGFVGLAAQLSQTWRVGYDVTSGFRVPNASE 516
 LYLSL---SQLYTPQTNLDADGKL----LKPR-----QGNQFEVGYKGSYMDDRLNAR 551
 VS------FYRMKDKNAAAPLNPNNKKTRYAA--LGKRVMEGVE-----TEIS 591
 283; Gaps
 14 AATVLAALSSSVFAAQTADLET------VHIKGQRSYNAIVTEKNGDYSSFAVTVGT
 168 RDLLLPEROFGVMMKNGYSTRNREWTNTLGFGVSNDRVDAALLYSORRGHETESAGKRGY
 276 GOGGHNYTVEESYNLLASYWREADDVNRRRNTNLFYEWTPESDRLSMVKADVDYQKTKVS
 DB 4; Length 791;
 Indels
 Version #1.30
 Query Match
4.9%; Score 186.5; DB 4;
Best Local Similarity 19.4%; Pred. No. 2.4e-08;
Matches 172; Conservative 103; Mismatches 329;
 HYKIESGE-GKTLHKASKT----KFTGYAGAV-----
 A-----VNYKGSFPTNYTTWETEYHKKEVGEIY
 ATTORNEY/AGENT INFORMATION:
NAME: No. 6277382nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 94,784-J
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-913-0001
INPORMATION FOR SEQ ID NO: 4:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,707
FILING DATE: 19-AUG-1997
 SEQUENCE CHARACTERISTICS:
LENGTH: 791 amino acida
TYPE: amino acid
 , MOLECULE TYPE: protein US-08-817-707-4
 CLASSIFICATION: 424
 TOPOLOGY:
```

| INFORMATION FOR SEQ ID NO: 2:  SEQUENCE CHARACTERISTICS:  LENGTH: 792 amino acids  i TYPE: amino acids  i TYPE: amino acid  TOPOLOGY: linear  MOLECULE TYPE: protein  US-08-326-670A-2  Query Match Best Local Similarity 19.6%; Pred. No. 3.3e-08;  Matches 173; Conservative 101; Mismatches 335; Indels 274; Gaps 39;  Matches 173; Conservative 101; Mismatches 335; Indels 274; Gaps 39;  Qy 14 AATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDVSSFAVTVGT 64                                                                                                                                                               | 326-670A- ence 2.7 ppliCANT: ppliCANT: ppliCANT: ppliCANT: ppliCANT: ppliCANT: iTLE OF I UMBER OF ORRESPOND ADDRESSE CITY: CITY: CITY: COUNTRY: COUNTRY: COMPUTER 6 MEDIUM I COMPUTER 6 MEDIUM I COMPUTER 7 MEDIUM I COMPUTER 7 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I COMPUTER 8 MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MEDIUM I MED | Db 576 VSGTPGCTEEDAYYYRCSDPYKEKLDWQMKNIDKARIRGIELTGRLNVDKVA 627  Qy 592 GAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANL 633    Color |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------|
| US-08-990-470A-2  JSequence 2, Application US/08990470A  Patent No. 6123942  Patent No. 6123942  GENERAL INFORMATION: APPLICANT: Stojiljkovic, Igor APPLICANT: Stojiljkovic, Igor APPLICANT: No. Magdalene  APPLICANT: Heffron, Fred  APPLICANT: Nassif, Xavier  TITLE OF INVENTION: No. 6123942el Bacterial Hemoglobin Receptor  TUTLE OF INVENTION: Genes and Uses  NUMBER OF SEQUENCES: 5  CORRESPONDENCE ADDRESS: ADDRESSE: MCDonnell Boehnen Hulbert & Berghoff  STREET: 300 South Wacker Drive, 32nd Floor  CITY: Chicago STATE: Illinois COUNTRY: USA ZIP: 60606  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk | Db 336 AVNYKGSPIEDSSTITRNÝNOKĎLĎEIÝ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Db 121 RYGNENSSRLSIDPELVRNIDIVKGADSENTGSGALGGGVNYQTLQG 167  Qy 177PTKAFQGHAAAGFGT                                               |

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NAME: No. 6277382nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 94,78
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
 ; Sequence 2, Application US/08817707; Patent No. 6277382
 E: Floppy disk
IBM PC compatible
 596 PKWQIHAGYSYLHSQ-----
 ATTORNEY/AGENT INFORMATION:
 792 amino acida
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 19-AUG-199
 TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER.ESTICS:
 , MOLECULE TYPE: protein US-08-817-707-2
 ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 CLASSIFICATION: 424
 COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PATENTI
 Chicago
Illinois
 amino acid
 GENERAL INFORMATION
 USA
 ADDRESSEE:
 TOPOLOGY:
 COUNTRY:
 RESULT 16
US-08-817-707-2
 STREET:
 LENGTH:
 STATE:
 638
 969
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 39;
 61 IKQEMIRDNKDLVRYSTDVGLSDSGRHQKGFAVRGVEGNRVGVSIDGVNLPDSEENSLYA 120
 RGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKR- 176
 ----PTKAF-----QGHA------AAGFGT---------HKQY 195
 KAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYL 255
 276 GQQGHNYTVEESYNLLASYWREADDVNRRRNTNLFYEWTPESDRLSMVKADVDYQKTKVS 335
 ---- 369
 DFENLNRDDYYFSGRVVRTISSIQHPVKTTM---YĞFSLSDQIQMNDVFSSRAĞIRYDHT 459
 520 FTYNHGSGNWLPNPNLKAERTTTHTLSLQGRSEKGTLDANLYQSNYRNFLSEEQKLTTSG 579
 65 KIPASLREIPQSVSIITNOQVKDRNVDTFDQLARKTPGLRVLSNDDG------RSSVYA 117
 168 RDLLLPERQFGVMMKNGYSTRNREWTNTLGFGVSNDRVDAALLYSQRRGHETESAGKRGY 227
 228 PVEGAGŚĠA-NIRĠŚARĠ-----IPDPSQ--HKYHSFLGKIAYQINDNHRIGASLN 275
 256 YOORH------LAPYNGLPADANNK-----LPSLPQHVFVGA--DWNKFKMN 294
 295 SHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACA 354
 355 VGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALN 414
 ----TRFKRITLRLD---SHPLQLGG-------GRHRLSFKTFASRR 402
 EFRSIPQVDLIANAR--KGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHY 472
 KIESGE-GKTLHKASKTK------FTGYAGAVYDLN------DNNSLYL--SLSQLY 514
 460 KMTPOELNAECHACDKTPPAANTYKGWSGFVGLAAQLNOAWRVGYDITSGYRVPNASEVY 519
 -----TPQTNLDAD-----GKLLK-PRQGNQFEVGYKGSYMDDR---LNA 550
 RVS-----FYRMKDKNAAAPLNPNNKKTRYAA--LGKRVMEGVE-----TEISGAVT 595
 Gaps
 14 AATVLAALSSSVFAAQTADLET------VHIKGQRSYNAIVTEKNGDYSSFAVTVGT 64
 Query Match
4.8%; Score 183; DB 3; Length 792;
Best Local Similarity 19.6%; Pred. No. 5.1e-08;
Matches 173; Conservative 101; Mismatches 335; Indels 274;
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 A----VNYKGSFPIEDSSTLTRNYNQKDLDEIY-----
 ATTORNEY AGENT INFORMATION:
NAME: NO. 6123942nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 94,784-K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 amino acids
TYPE: amino acid
 APPLICATION NUMBER: US/08/990,470A
FILING DATE: 15-DEC-1997
CLASSIFICATION: 536
 TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-990-470A-2
 121
 196
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39;
 633 EGWKLFGSLGYAKSKLSGDNSLLSTQPLKVIAGIDYESPSEKWGVFSRLTYLGAKKVKDA 692
 61 IKQEMIRDNKDLVRYSTDVGLSDSGRHQKGFAVRGVEGNRVGVSIDGVNLPDSEENSLYA 120
 118 RGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKR- 176
 121 R---YGNFNSSRLSIDPELVR-----NIDIVKGADSFNTGSGALGGGVNYQTLQG 167
-----IKTASNSRDDGIFLLMPKHSANLWTTY 637
 693 OYTVYENKGWGTPLOKKVKDYPWLNKSAY-VFDMYGFYKPVKNLTLRAGVYNVFNRKYTT 751
 65 KIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDG-----RSSVYA 117
 Indels 274; Gaps
 14 AATVLAALSSSVFAAQTADLET-----VHIKGQRSYNAIVTEKNGDYSSFAVTVGT 64
 OVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY--
 APPLICANT: Stojiljkovic, Igor
APPLICANT: Stojiljkovic, Igor
APPLICANT: Hwa, Vivian
APPLICANT: Hweffron, Pred
APPLICANT: Hweffron, Pred
APPLICANT: Nassif, Xavier
TITLE OF INVENTION: No. 6277382el Bacterial Hemoglobin Receptor
TITLE OF INVENTION: Genes and Uses
CORRESPONDENCES: 15
 Length 792;
 -----YARVG-----GANTFNIPGSERTWTANLRYSF 722
 |: : | : : | : 1 | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... |
 B: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive, 32nd Floor
 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
 Query Match

4.8%; Score 183; DB 4; L
Best Local Similarity 19.6%; Pred. No. 5.1e-08;
Matches 173; Conservative 101; Mismatches 335;
 MBER: US/08/817,707
19-AUG-1997
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 RESULT 17
US-08-628-434-4
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 Sequence 4, Application US/08628434 Patent No. 6265567
 GENERAL INFORMATION:
APPLICANT: Sparling, P. Frederick
APPLICANT: Beucher, Margaret
TITLE OF INVENTION: Isolated FrpB Nucleic
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: INClone Systems Incorporated
STREET: 180 Varick Street
 ZIP: 10014

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/628,434
 752
 633
 551
 520
 460
 473
 403
 415
 355
 276
 256
 177
 168
 STATE: N
COUNTRY:
 CITY: New York
STATE: New York
 WDSLRGLYSYSTINSVDRDGKGLDRYRAP--SRNYAVSLEWKF 792
 PKWQIHAGYSYLHSQ-----
 DVSCTQMNYYYGMCS-----NPYSEKLEWQMQNIDKARIRGLELTGRLNVDKVASFVP
 RVS-----FYRMKDKNAAAPLNPNNKKTRYAA--LGKRVMEGVE----TEISGAVT
 FTYNHGSGNWLPNPNLKAERTTTHTLSLQGRSEKGTLDANLYQSNYRNFLSEEQKLTTSG
 DFENLNRDDYYFSGRVVRTTSSIQHPVKTTN---YGFSLSDQIQWNDVFSSRAGIRYDHT
 EFRSIPQVDLIANAR--KGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHY 472
 ----TRFKRITLRLD---SHPLOLGG-------GRHRLSFKTFASRR
 VGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALN
 A----VNYKGSFPIEDSSTLTRNYNOKDLDEIY-------NRSMD----
 SHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACA 354
 YQQRH-----LAPYNGLPADANNK-----LPSLPQHVFVGA--DWNKFKMN 294
 -----YARVG------GANTFNIPGSERTWTANLRYSF 722
 QYTVYENKGWGTPLQKKVKDYPWLNKSAY-VFDMYGFYKPVKNLTLRAGVYNVFNRKYTT
 QVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY--
 EGWKLFGSLGYAKSKLSGDNSLLSTOPLKVIAGIDYESPSEKWGVFSRLTYLGAKKVKDA
 -----TPQTNLDAD-----GKLLK-PRQGNQFEVGYKGSYMDDR---LNA 550
 KMTPQELNAECHACDKTPPAANTYKGWSGFVGLAAQLNQAWRVGYDITSGYRVPNASEVY
 KIESGE-GKTLHKASKTK-----FTGYAGAVYDLN-----DNNSLYL--SLSQLY 514
 GOOGHNYTVEESYNLLASYWREADDVNRRRNTNLFYEWTPESDRLSMVKADVDYQKTKVS
 PVEGAGSGA-NIRGSARG-----IPDPSQ--HKYHSFLGKIAYQINDNHRIGASLN
 KAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYL 255
 RDLLLPEROFGVMMKNGYSTRNREWTNTLGFGVSNDRVDAALLYSORRGHETESAGKRGY 227
 ----PTKAF-----QGHA------AAGFGT-----
 USA
 US/08/628,434
 Version
 - IKTASNSRDDGIFLLMPKHSANLWTTY
 Acid Molecule
 ----HKQY 195
 579
 459
 275
 692
 632
 519
 414
 335
 637
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 Vaccine
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 US-08-628-434-4
 Query Match
Best Local Similarity
Matches 171; Conserv
 TELEFAX: (212) 645-205
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 PILING DATE: 07-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gallagher, Thomas C.
REGISTRATION UNMBER: 37,066
REFERENCE/DOCKET NUMBER: SPA-
TELECOMMUNICATION INFORMATION:
 MOLECULE TYPE: protein
 FILING DATE: 05-APR-:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
 630
 577
 435
 378
 429
 388
 347
 202
 301
 165
 244 INPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWN----KFKMNSHDVFA
 135
 186
 128
 318 ADDKDNGYAGNVKGPNHTRIATRGMNFNFDSRLAEQTLLKYGINYRHQEIKPQAFLNSQF
 86
 TYPE: amino acid
 46
 89
 TOPOLOGY:
 LENGTH:
 TELEPHONE:
 æ
 DRFKVKTHDGKTV---SSSSLNPSFGVIWQPREHWSFSASHNYASRSPRLYDALQTHGKR
 KIEDKKDATEEDKKKNRENEKIAKAYRLTNPTKT--DTGAYIEA-IHEIDGFTLTGGLRY
 DLKHYFGNGGYGKVG----MRYSDRDADSNYAFAGSKLG-----MKTPAGRPGCN
 AAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASP--RPAEKNNRHETFYAAADWD 243
 DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVN--LVRKRPTKAFQGHA 185
 FRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIP 67
 ALGKRVMEGVETEISGAVTPKWQIHAGYSYLH-----SQIKTASNSRDDGIFLLMPKH--
 GIISIADG--TKAERARNTEIGF--NYNDGTFAANGSYFRQTIKDALA--NPQNR-----
 ---LDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYA
 GHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSL----YLSLS-QLYTP-QTN---
 GADYNRFRSTNEQG--RTTLYARG-----
 TVREEFAVGGENSRITIKRQAPAYRETTQSNTNLAYTGKDLGFVEKLDANAYVLEKKRYS
 TADDKACAVGLGTE--IKQKALAFDASYSRPFRLGNT------ANEFVI-----
 --KDYEAGKGFRNVNGGKTVPYSALDKRSYLAKIGTTFGDGDHRIVLSHMKDQ--HRGIR
 VR----LNSGF-----AGNNGVSYGAS------VF-GKEGNFDGLFSYNRNDE--
 ----RTNIVTLOOKDESTATDMRELLKEEPSIDFGGGNGTSOFLTLRGMGQNSVDI
 ASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNI 127
 FRISILSLTLAAGFAHAAENNANVALDTVTVKGDRQ-----
 713 amino acids
 4.8%; Score 181; DB 4; Length 713; ilarity 20.3%; Pred. No. 6.6e-08; Conservative 110; Mismatches 279; Indels 2
 (212) 645-2054
 (212) 645-1405
 ----HDSVAVREAVNAGYIKNHGYELGASYRTGGLTAKVGVSRSKPRFYD
 05-APR-1996
 ----KGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRL
 -----KVDNAYSDSQILYHQGRF--IVDPALVKVVSVQKGAGSA
---LWT---TYQV-TPELTIGGG---VNAMSGITSSAGMH----
 US 08/418,964
 4:
 --GATNGAIIAKTVDAQDLLKGLDKN
 -GLALNEFRSIPQVDLIANA
 -----GSKI- 45
 ------WG
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434 469 377 428

540

491 519 346

317 387 257 300 164

201

134

97

Gaps

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è
 31;
| |:| |
----PHSQR-W 694
 -----AGGYATFDAMAAYRFTPK--LKLQINADNIFNRHYYARVGGANTFNIPGSERTW 714
 Gaps
 -----LREIPQSVSIITNQQVKDRNVD 91
 APPLICANT: Children's Hospital & Medical Center
APPLICANT: University of Washington
APPLICANT: Washington State University Research Foundation
APPLICANT: TARK, PHILIP I
APPLICANT: BESSER, THOMAS E
APPLICANT: BESSER, THOMAS E
APPLICANT: VARY JR, JAMES C
TITLE OF INVENTION: ESCHERICHIA COLI 0157:H7 EPITHELIAL ADHESIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
 Query Match 4.8%; Score 180.5; DB 5; Length 718; Best Local Similarity 18.8%; Pred. No. 7.4e-08; Matches 146; Conservative 92; Mismatches 285; Indels 255;
 E: CHRISTENSEN, O'CONNOR, JOHNSON AND KINDNESSPLLC SUITE 2800, 1420 FIFTH AVENUE
 TOPOLOGY: linear MOLECULE TYPE: protein DESCRIPTION: Vibrio cholerae IrgA amino acid sequence, DESCRIPTION: wherein Xaa" residues represent gaps DESCRIPTION: introduced to facilitate best alignment with DESCRIPTION: SEQ ID NO:6.
 |: | : : : | | : | | 647 KLENVVRQGFGVNDVFANWKPLGKDTLNVNLSVNNVFDKFYY---
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PPLICATION NUMBER: PCT/US95/06994 FILING DATE: 07-JUN-95
 PILING DATE: ...

CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/265,714
FILING DATE: 24-UNA-1994
ATTORNEY/AGENT INFORMATION:
NAME: BRODERICK, THOMAS F
REFERENCE/DOCKET NUMBER: 31.332
REFERENCE/DOCKET NUMBER: CHOR-18591
TELEPHONE: (206) 682 8100
TELEPHONE: (206) 682 8100
TELEPHONE: (206) 244 0779
INFORMATION FOR SEQ 1D NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acids
TYPE: amino acids
TYPE: ...
TYPE: ...
 ADDRESSEE: CHRISTENSEN, O'CONNOR, STREET: SULTE 2800, 1420 FIFTH AVE CITY: SEATTLE STATE. WASHINGTON COUNTRY: USA ZIP: WAS 98101 COMPUTER READABLE FORM: MEDIUM TYPE: FLORPY disk COMPUTER: IBM PC COMPALISE: DOPERATING SYSTEM: PC-DOS/MS-DOS
 sequence 7, Application PC/TUS9506994 GENERAL INFORMATION:
 VIBRIO CHOLERAE
 57 SFAVTVGTKIPAS-----
 HYPOTHETICAL: N
ORIGINAL SOURCE:
ORGANISM: VIE
 715 TANL 718
 TNTL 698
 RESULT 18
PCT-US95-06994-7
; Sequence 7, App
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| TYPE: FI<br>ER: IBM F                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ΣΫ               |  |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------|--|
| 060                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                  |  |
| STATE: Illinois<br>COUNTRY: USA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | is d             |  |
| STREET: 300 South Wacker Drive, 32nd Floor<br>CITY: Chicago                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ກ ເປັ<br>• • • • |  |
| DENCE ADDRESS:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | COK              |  |
| OF SEQUENCES: 14                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | MON :            |  |
| INVENTION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | itit ;           |  |
| Hef                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | APPI             |  |
| So, Magdalene<br>Hwa, Vivian                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | , APPI           |  |
| GENERAL INFORMATI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 5                |  |
| equence 2,<br>atent No.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Sec              |  |
| ULT 19<br>08-537-361E-2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 58               |  |
| 616 GKXXXEMQPEGGASNDDFIAPXXXXXXXXXXITFIDTGVTYALTDTATIKAAVYNLFDQ 673                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Db 61(           |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Qy 65            |  |
| :  ::        ::          :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Db 558           |  |
| 593 AVTPKWQIHAGYSYLHŞQIKTASNSRDDGIFLLMPKHSANLWTYQVTPELTIGGGVNAM 652                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 0y 59:           |  |
| 505LTAPHNDFXDKITRVACPANICTAGPNQWGATPTYRVNIDBABTYGABATLSL 557                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Db 50!           |  |
| 541 GSYMDDRLNARVSFYRMKDKNRAAPLNPNNKKTRYAALGKRVMEGVFTEISG 592                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Qy 54:           |  |
| 462 PDWGQVSGGGXXXIYGNPDLQPETSINKELSLMYSTGSGLAAS504                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Db 46:           |  |
| - <b>,</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Qy 49:           |  |
| 418EDHDKNYG-SHFSPRVYGVWNLDPLWTVKGGFRAPQLREVT 461                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Db 418           |  |
| 440 ATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFT- 491                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Oy 44(           |  |
| 380 KTSNKISSRTHISNTQW4GFIEDEWALAEQFRLTFGGR 417                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Db 38(           |  |
| 380 NTANEFVIGADYNRFRSTNEQGRITLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTV 439                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Qy 38(           |  |
| 344 XXMSIDNIVFKSTLVAPIGEHMLSFGVEGKHESLED 379                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Db 34            |  |
| 326NYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLG 379                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Qy 320           |  |
| 301 QGDWQGVXGQSDTYLQYEENTNKSREXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | .0E qa           |  |
| 286 -ADMUKFKMISHDVFADLKHYFGNGGYGKVGMRYSDRDADS 325                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Qy 28            |  |
| 243 QLNPDHQLQLEAGVSAQDRENNVGKSAQSSGCXXXXXXRGTCSNTDNQYRRNHVAVSH 300                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Db 24:           |  |
| 243 DINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG- 285                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Oy 24:           |  |
| 190 GDEQSANFFVTGPL-SDXALSLQVYGQTTQRDEDEIEHGYGDKSLRSLTSKLNY 242                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Db 19            |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Qy 18            |  |
| 130 QGWLPPLQAIERIEVIRGPMSTLYGSDAIGGVINIITRKDQQQWSGNVQLSTVVQENRAS 189                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Db 13            |  |
| 138 NGTLPNLPAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAA 187                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Qy 13(           |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 7 da             |  |
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 INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 amino acids
TYPE: amino acids
TOPOLOGY: linear
 US-08-537-361E-2
 Best Loca
Matches
 Query Match
 ATTORNEY/AGENT INFORMATION:
NAME: NO. 6121037nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 94,784-A
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,361E
FILING DATE: 02-OCT-1995
CLASSIFICATION: 536
 TOPOLOGY: linear MOLECULE TYPE: protein
 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-913-0001
 196
 177
580 DVSCTQMNYYYGMCS-----NPYSEKLEWQMQNIDKARIRGIELTGRLNVDKVASFVP 632
 460
 473
 403
 370
 336 A----VNYKGSFPIEDSSTLTRNYNOKDLDEIY---
 168 RDLLLPEROFGVMMKNGYSTRNREWTNTLGFGVSNDRVDAALLYSORRGHETESAGKRGY 227
 121 R---YGNFNSSRLSIDPELVR-----NIDIVKGADSFNTGSGALGGGVNYQTLQG 167
 118
 551 RVS-----FYRMKDKNAAAPLNPNNKKTRYAA--LGKRVMEGVE-----TEISGAVT 595
 355 VGLGTBIKOKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEOGRTTLYARGGLALN 414
 295 SHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACA 354
 276 GOOGHNYTVEESYNLLASYWREADDVNRRRNTNLFYEWTPESDRLSMVKADVDYOKTKVS
 256 YQQRH-----LAPYNGLPADANNK-----LPSLPQHVFVGA--DWNKFKMN 294
 228 PVEGAGSGA-NIRGSARG------IPDPSQ--HKYHSFLGKIAYQINDNHRIGASLN 275
 61
 65
 10
 14 AATVLAALSSSVFAAQTADLETVHI------KGQRSYNAIVTEKNGDYSSFAVTVGT 64
 7. Match 4.8%; Score 180; DB 3; Length 792; Local Similarity 19.4%; Pred. No. 9.7e-08; 172; Conservative 104; Mismatches 328; Indels 2
 TELEPHONE: 312-5.
TELEPHONE: 312-913-0002
 KAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYL 255
 DFENLNRDDYYFSGRVVRTTSSIQHPVKTIN---YGFSLSDQIQWNDVFSSRAGIRYDHT 459
 EFRSIPQVDLIANAR--KGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHY 472
 IKQEMIRDNKDLVRYSTDVGLSDSGRHQKGFAVRGVEGNRVGVSIDGVNLPDSEENSLYA 120
 KIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDG-----RSSVYA 117
 KIESGE-GKTLHKASKTK-----FTGYAGAVYDLN-----DNNSLYL--SLSQLY 514
 RGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKR- 176
 AALVGSIFGNEVFAADEAATETTEVKAEVKAVRGKGQRNAPAAVER------VNLNR 60
 FTYNHGSGNWLPNPNLKAERTTTHTLSLQGRSEKGTLDANLYQSNYRNFLSEEQKLTTSG
 ----TPQTNLDAD-----GKLLK-PRQGNQFEVGYKGSYMDDR---LNA 550
 KMTPQELNAECHACDKTPPAANTYKGWSGFVGLAAQLNQAWRVGYDITSGYRVPNASEVY
 ----TRFKRITLRLD---SHPLQLGG-----
 ----- 369
 Indels 284; Gaps
 --GRHRLSFKTFASRR 402
 579
 519
 335
 42;
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|   | Ş                                    | 596 PKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTY 637                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|---|--------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|   | 망                                    | 633 EGWKLFGSLGYAKSKLSGDNSLLFTQPLKVIAGIDYESPSEKWGVFSRLTYLGAK 687                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|   | Ş                                    | 638QVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFN 692                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|   | 뮍                                    | 688 KVKDAQYTVYENKGWGTPLQKKVKDYPWLNKSAY-VPDMYGFYKPVKNLTLRAGVYNVFN 746                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|   | \$ 8                                 | 93 RHYYARVGGANTENIFGSERTWTANLRYSF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|   | ઠ                                    | 747 RKYTTWDSLRGLYSYSTINSVDRDGKĞLDRYRAPSRNYAVSLEWKF 792                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | RESULT<br>US-08-<br>; Sequ<br>; Pate | RESULT 20<br>US-08-537-361E-6<br>; Sequence 6, Application US/08537361E<br>; Patent No. 6121037                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|   | <br>ല്ല                              | INFOR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|   |                                      | Hwa, Vivi                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|   | ٠. ٠.                                | Xavier                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   |                                      | NVENTION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|   |                                      | QUENCES: 14                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|   |                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|   | ٠. ٠.                                | 발                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|   |                                      | ZIP: 66066 COMPUTER READABLE FORM:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|   |                                      | MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOOCAGE COMPUTER: TOO |
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|   |                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|   | ٠                                    | Y/AGENT INFORMATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|   |                                      | ,303                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|   |                                      | PΙ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|   | <br>IJ                               | INFORMATION FOR SEQ ID NO: 6:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|   |                                      | CHARACTERISTICS: 792 amino acids                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|   | 80-Sn                                | TOPOLOGY: 1i MOLECULE TYPE: -537-361E-6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| • | Quer<br>Best<br>Matc                 | 4.7%; Score 179; DB 3; Length 792;<br>Best Local Similarity 19.8%; Pred. No. 1.2e-07;<br>Matches 175; Conservative 96; Mismatches 338; Indels 274; Gaps 40;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|   | Ş                                    | 14 AATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGT 64                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|   | ઠ                                    | 10 AALVGSIFGNPVFAADEAATETTPVKAEVKAVRVKGQRNAPAAVERVNLNR 60                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|   | Ş                                    | 5 KIPASLREIPQSV8IITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA 11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|   | ? 5                                  | TARENT TRAITCOME TO TO TO THE THE TIME THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRAITCOME TO THE TRA |
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135 SAGI------WGATNGAIIAKTVDAQDLLKGLDKN------WG 164
 244 INPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWN---KFKMNSHDVFA 300
 - KDYEAGKGFRNDNGGKTVPYSALDKRSYLAKIGTTFGDGDHRIVLSHMKDQHRGIRTV 259
 -----ADSNYAFAGSKLGM--KTPAG----RPGCNTAD 349
 -NRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATENLDEFGIY 450
 380 KDKEKATNEEKKKN------RENEKIAKAYRLTNPTK-------TDDTGAY 416
 604 YSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQVT-----PELTIGGG---VNAMS 653
 68 ASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNI 127
 -------KVDNAYSDŠQILYHQGRF--IVDPALVKVVSVQKGAGSA 134
 DKACAVGLG-----TEIKQKALAFD------ASYSRPFRLGNTANEFVIGADY-- 391
 8 FRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIP 67
 FRISILSLTLAAGFAHAAENNANVALDTVTVKGDRQ--------GSKI- 45
 128 DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVN--LVRKRPTKAFQGHA
 186 AAGFGTHKOYKAEADVSGSLNSDGSVRGRVMAQTVGASP--RPAEKNNRHETFYAAADWD
 VR----LNSGF-----AGNNGASYGASVF-GKEGNFDGLFSYNRNDE--
 301 DLKHYFG-----NGG-----YGG----YGKVGMRYSDRD------
 GKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKPTG------YA
 G---AVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNAR
 552 VSFYRMKDKNAAAPLNPNNKKTRYAA----LGKRVMEGVETEIS---GAVTPKWQIHAG
 523 GSYFRQTIKDALA--NPQNRHDSVAVREAVNAGYIKNHGYELGASYRTGGLTAK----VG
 Query Match
4.6%; Score 173; DB 4; Length 713;
Best Local Similarity 19.0%; Pred. No. 3.7e-07;
Matches 163; Conservative 107; Mismatches 277; Indels 310;
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/418,964
FILING DATE: 07-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gallagher, Thomas C.
REGISTRATION NUMBER: 37,066
REFERENCE/DOCKET NUMBER: SPA-3-P
TELECOMMUNICATION:
TELEPHONE: (212) 645-1405
 TELEPHONE: (212) 645-1405
TELEPAX: (212) 645-2054
INPORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
 LENGTH: 713 amino acids TYPE: amino acid
 , MOLECULE TYPE: protein US-08-628-434-2
 TOPOLOGY:
 LENGTH:
 46
 98
 165
 202
 350
 320
 392
 195
 323
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 596 PKWQIHAGYSYLHSQ------IKTASNSRDDGIFLLMPKHSANLWTTY 637
 SHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACA 354
 <u> OYTVYENKGWGTPLOKKVKDYPWLNKSAY-VFDMYGFYKPVKNLTLKAGVYŇVFNRKYTT 751</u>
 | | : : : : | : : : | | . : : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | | . : : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . :
 DVSCTQMNYYGMCS-----NPYSEKLEWQMQNIDKARIRGIELTGRLNVDKVASFVP
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 RDLLLPERQFGVMMKNGYSTRNREWTNTLGFGVSNDRVDAALLYSQRRGHETESAGKRGY
 KIESGE-GKTLHKASKTK-----FTGYAGAVYDLN-----DNNSLYL--SLSQLY
 APPLICANT: Sparling, P. Frederick
APPLICANT: Beucher, Margaret
TITLE OF INVENTION: Isolated FrpB Nucleic Acid Molecule
NUMBER OF SEQUENCES: 4
CORRESPONDENCES. ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
 -----YARVG-----GANTFNIPGSERTWTANLRYSF 722
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 COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-APR-1996
 STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: USA
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 Sequence 2, Application US/08628434 Patent No. 6265567
 PVEGAGSGA-NIRGSARG-
 GENERAL INFORMATION:
 US-08-628-434-2
 168
 . 952
 295
 460
 280
 752
 196
 228
 336
 370
 419
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 473
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 RESULT 22
US-08-613-009A-18
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 US-08-613-009A-18
 Patent No.
 Sequence 18,
 Matches
 Query Match
 GENERAL INFORMATION: APPLICANT: Myers,
 TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
 APPLICANT:
 REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
 SEQUENCE CHARACTERISTICS:
 FILING DATE: 08-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 CORRESPONDENCE ADDRESS
 APPLICANT: Yang, Y
APPLICANT: Klein,
TITLE OF INVENTION:
 APPLICANT:
 NUMBER OF SEQUENCES:
 APPLICANT:
 159
 101
 577
 654 GITSSAGMH------AGGYATFDAMAAYRFTPK--LKLQINADNIFNRHYYARVGG 701
 58
 TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
 LENGTH:
 COMPUTER: IBM PC
OPERATING SYSTEM:
 Local Similarity
 NAME: Stewart, Michael
 APPLICATION NUMBER:
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 ADDRESSEE:
LFDSSGEMGGIVNLVRKRPTKAFQGHAAAG-FGTHKQYKAEADVSGSLNSDGSVRGRVMA 217
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 QQQHLFRLNILCLSLMTALPAYAENVQAGQAQEKQLDTIQVKAKKQKTRRDNEVTG---- 57
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 -RGYEYSEYN--IDGLPAQMQS-----INGTLP-----NLFAFDR---VEVMRGPSG 158
 RY: Canada
M5G 1R7
 9, Application US/08613009A
6090576
 Toronto
 Ontario
 6th Floor,
 915 amino acids
 -PHSQR-WINTL 698
 Klein, Michel H
VENTION: Transferrin Receptor
 Schryvers, Anthony B
Harkness, Robin E
Loosmore, Sheena M.
 Conservative
 Yang, Yan-Ping
 Du, Run-Pan
 Myers, Lisa E
 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
 Sim & McBurney
 LGKLVKTADTLSKEOVLD-----IRDLTRYDPGIAVVEQGRGASSGYS 100
 single
 4.6%; Score 173; DB 3; L
21.4%; Pred. No. 5.5e-07;
tive 99; Mismatches 292;
 330 University Avenue
 US/08/613,009A
 1038-542
 Genes
 #1.30
 Length 915;
 of.
 Indels
 Moraxella
 242;
 Gaps
 57
 633
 43;
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RESULT 23
US-08-778-570B-24
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 Sequence 24, Application US/08778570B Patent No. 6437096
 GENERAL INFORMATION:
 COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
 APPLICANT:
APPLICANT:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,570
 APPLICANT:
 CORRESPONDENCE ADDRESS
 TITLE OF INVENTION: NUMBER OF SEQUENCES:
 APPLICANT:
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FILING DATE:
 STATE:
 CITY: Toronto
 STREET:
 ADDRESSEE:
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 Ontario
 6th Floor,
 Klein, Michel H
 Yang, Yan-Ping
 Du, Run-Pan
 Loosmore,
 Harkness, Robin
 Schryvers,
 Myers, Lisa E
 Sim & McBurney
Sim & McBurney
A Floor, 330 University Avenue
03-JAN-1997
 Transferrin : 43
 Sheena M.
 US/08/778,570B
 ---HKLLQAAFKKSFDTAKIRHNLSVNLGYDRFGSNLRHQD
 -AFQTKTADDVIGEGRQWGIQSKTAYSGKNRGLTQSLALA
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 of Moraxella
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 617
 568
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 504
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 401
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655 -EMYGWRSGDKIKAVKIDPEKSFNK 678
 Query Match
 159
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 118
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 43;
 -----LGKLVKTADTLSKEQVLD----IRDLTRYDPGIAVVEQGRGASSGYS 100
 217
 58 FAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA 117
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 -PADLKHYFGNGGYGKVGMRYSDRDA-----DSNYAFAGSKLGMKTPAGR---P 343
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 -----HKLLQAAFKKSFDTAKIRHNLSVNLGYDRFGSNLRHQD 514
 505 SLYLSLSQLYTPQTNLDADGKLLKP--RQGNQPEVGYKGSYMDDRLNARVSFYRMKDKNA 562
 569 YTDCTPRSINGKSYYAAVRDNVRLG------RWADVGAGIRYDYRSTHSDDGSVS 617
 613 TASN---SRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATF 669
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 GCNTADDKACAVG--LGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQG 401
 RTTLYARGGLAL-NEFRSIPQVDLIANARKGVRGYSHTVATENLDEFG----1YGKSTFH 456
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 ---TSTGFRLPSFA-- 654
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 2 QQQHLFRLNILCLSLMTALPAYAENVQAGQAQEKQLDTIQVKAKKQKTRRDNEVTG----
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 515 YYYQSANRAYSSKTPPQNNGKKTSPNGREKNPYWVSI-----GRGNVVTRQICLFGNNT
 160 VEQGSGALAGSV-----AFQTKTADDVIGEGRQWGIQSKTAYSGKNRGLTQSLALA
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 GLFTSGENNAPVGAEYGTGVFYDETHTKSRYGLEYVYTNADKD--TWADYARLS----
 QTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPY------
 Query Match
4.6%; Score 173; DB 4; Length 915;
Best Local Similarity 21.4%; Pred. No. 5.5e-07;
Matches 172; Conservative 99; Mismatches 292; Indels 242;
 ---NGLPADANNKLPSLPQHVFVGADW-------SNKFKMN--SHDV----
 PADGLSLIGGGRLGHYKIESGEGKTLHKASKTKF----
 1038-664
 618 rGTHRTLSWNAGIVL --- KPADWLDLTYR-
 DAMAAYRFTPKLK-LQINADNIFNR 693
 ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038
TELECHONINICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-778-570B-24
 CLASSIFICATION:
 58
 218 (
 45.7
 265
 378
 402
 211
 299
 344
 670
 477
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43;
 160 VEQGSGALAGSV------AFQTKTADDVIGEGROWGIQSKTAYSGKNRGLTQSLALA 210
 58 PAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA 117
 -----LGKLVKTADTLSKEÓVLĎ----IRDĽTRYDPGIAVVEQGRGAŠSGYS 100
 -RGYEYSEYN--IDGLPAQMQS-----INGTLP-----NLFAFDR---VEVMRGPSG 158
 LFDSSGEMGGIVNLVRKRPTKAFQGHAAAG-FGTHKQYKAEADVSGSLNSDGSVRGRVMA 217
 3 OFMSVFRIN---MTAATVLAALSSSVFA--AQTABLETVHIKGQRSYNAIVTEKNGDYSS 57
 APPLICANT: Harkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Loosmore, Sheena M.
APPLICANT: Vang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
CORRESPONDENCE: 60
CORRESPONDENCE ADDRESS:
 4.6%; Score 173; DB 4; Length 915; 21.4%; Pred. No. 5.5e-07; tive 99; Mismatches 292; IndelB 2
 MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
 3: Sim & McBurney
6th Floor, 330 University Avenue
 CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/778,570
FILING DATE: 03-JAN-1997
 UMBER: US/09/059,584
14-APR-1998
 Myers, Lisa E
Schryvers, Anthony B
Harkness, Robin E
Loosmore, Sheena M.
Du, Run-Pan
 Sequence 24, Application US/09059584; Patent No. 6440701; GENERAL INFORMATION:
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/POCKET NUMBER: 1036
TELECOMMUNICATION INFORMATION:
 (416) 595-1155
 TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2
 : 915 amino acida
amino acid
 CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
 Best Local Similarity 21.43
Matches 172; Conservative
 SEQUENCE CHARACTERISTICS
 SS: single
linear
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
 Abbacastrates of streets Toronto
 STRANDEDNESS:
 FILING DATE:
 TELEPHONE:
 ADDRESSEE:
US-09-059-584-24
 US-09-059-584-24
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RESULT 25
US-08-487-890A-96
 Sequence 96, Application US/08487890A Patent No. 5708149
 Patent No.
 GENERAL INFORMATION:
 APPLICANT:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PAID:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
 APPLICANT:
 APPLICANT:
 CORRESPONDENCE ADDRESS:
 STREET: STREET: Toronto
 569
 563
 515
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 402
 378
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 655 -EMYGWRSGDKIKAVKIDPEKSFNK 678
 218
 CLASSIFICATION:
 COUNTRY: Canada
ZIP: M5G 1R7
 ADDRESSEE:
 RFENKRHYIG-GILERTQQTFDTRDMTVPAFLTKAVFDANQKQAGSLRGNGKYAGNHKYG
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 TGTHRTLSWNAGIVL---KPADWLDLTYR--
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 AAPLNPN--NKKTRYAALGKRVMEGVETEISGAVTPKW-QIHAGYSY----LHS---QIK 612
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 Gray-Owen, Scott
Yang, Yan-Ping
Murdin, Andrew
 Chong, Pele
 Schryvers,
 Harkness, Robin
 Loosmore, Sheena
 Sim & McBurney
 07-JUN-1993
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 330 Unviersity Avenue
 Anthony
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US-08-487-890A-96
 Query Match 4.6%; Score 172; DB 1; L Best Local Similarity 21.4%; Pred. No. 6.9e-07; Matches 172; Conservative 100; Mismatches 291;
 TELEFAX: (416) 595-116
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 APPLICATION NUMBER: UPPLING DATE: 29-DEC-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UPPLICATION NUMBER
 REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
 FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
 569
 477
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 319
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 263
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 STRANDEDNESS:
TOPOLOGY: 1i
 58
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 TELEPHONE:
 NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
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 LENGTH: 915 amino acids
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TASN---SRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATF
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(416) 595-117
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 29-DEC-1993
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us-09-889-267-2.rai

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Patent No. 5922323<br>; GENERAL INFORMATIO | APPLICANT: LOOS |   | ; APPLICANT: Chon<br>; APPLICANT: Gray<br>. applicant: Vand | APPLICANT: Murd | Z                                                                         | CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT CONTENT | STREET: Suite                                                                                                                    | STATE: Ontari | ZIP: CARA ; ZIP: M5G 1R7 ; COMPUTER READABL                                                                                | MEDIUM TYPE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | O)                                                                    |
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| Db 618 TCTHRILSWNAGIVLKPADMIDLIYRTSTGFRLPSFA 654 | QINADNIFNR 693     | Db 655 -EMYGWRSGDKIKAVKIDPEKSFNK 678 | 20 Hittigan        | NESULI 26<br>US-08-363-124A-2 | ; Sequence Z, Application US/U83831Z4A<br>; Patent No. 5912336 | ; GENERAL INFORMATION:<br>; APPLICANT: Sparling, P. Frederick | sen, Cynthia N.<br>Transferrin-Binding | isseria Gonorrhea | CORRESPONDENCE ADDRESS: ADDRESSER: ImClone Systems Incorporated | É.  | 3 0 | ; COUNTRY: USA<br>; ZIP: 10014 | ER READABI         | MEDIUM 11FE: FICHPY WISK COMPUTER: ISM PC Compatible COMPUTER: PC PC VICE PC | SOFTWARE: PC-DOS/MS-DOS ; SOFTWARE: Patentin Release #1.0, Version #1.25 | CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/363,124A | ; FILING DATE: 23-DEC-1994<br>; CLASSIFICATION: 536 | ; PRIOR APPLICATION DATA:<br>; APPLICATION NUMBER: US 08/124,254 | ; FILING DATE: 20-SEP-1993<br>; PRIOR APPLICATION DATA: | APPLICATION NUMBER: US 07/973,336 | PRIOR APPLICATION DATE: | ; APPLICATION NUMBER: US 0//5/2,18/<br>; FILING DATE: 23-AUG-1990 | ; ATTORNEY/AGENT INFORMATION:<br>; NAME: Gallagher, Thomas C. | ; REGISTRATION NUMBER: 37,066<br>; REFERENCE/DOCKET NUMBER: SPA-1-PDC | 2 5              | 2 ~                                          | ,               | 랿 | ; TOPOLOGY: linear ; MOLECULE TYPE: protein                 | 4<br>.**7       | Similarity 21.4%; Pred. No. 6.9e-07; 2: Conservative 100: Mismatches 291; | יומרכוונים דייני ככווסטידימרידים בייניים בייניים בייניים פייניים ייניים פיינים  OY 3 CFMSVERINMIAATVEALESSVERAQTADLETVHIRGERSINALVIERAGUISS 5/<br>Db 2 OOOH-PPINALTGISMTALPAARNVOACAORKOLDTTOVKAKKKKRFRDNEVTG 57 |               | OY SO FAVIVELLIFABLEALE PEGASSITING VERNOTIFULARIA PELEVIDENSSO I II.  DD 58LGKLVKTADTLSKEOVLDIRDITRYDGIAVVEOGREASSGYS 100 | ODD DANKET WAS TRANSPORTED TO THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF T | - KGIBIOBIN IDGLENGIQOINGINENEPEREGEGOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG |

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Floppy disk
M PC compatible
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LTENTIN Release #1.0, Version #1.25
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 KLK-LQINADNIFNR 693
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995

US/08/478,435

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 TOPOLOGY: US-08-478-435-96
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 Query Match
Best Local Similarity
Matches 172; Conserv
 TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 96
 NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10.
TELECOMMUNICATION INFORMATION:
 APPLICATION NUMBER: US 01
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
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 FILING DATE: 29-DEC-1993
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 477
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TYPE: amino acid
STRANDEDNESS: sir
 88
 FILING DATE: 08 CLASSIFICATION:
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 CLASSIFICATION:
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 08-NOV-1994
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COMPUTER: IBM PC COMPATIBLE
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SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: 08 NOV-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 M
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
 GENERAL INFORMATION:
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 APPLICANT:
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 ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 CORRESPONDENCE ADDRESS
 APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
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 STREET: Suite CITY: Toronto
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 Ontario
 Application US/08337483
 Suite 701, 330 Unviersity Avenue
 915 amino acids
 Murdin, Andrew
Klein, Michel
 Gray-Owen, Sco
Yang, Yan-Ping
 Harkness, Robin
Schryvers, Anthony
 (416) 595-1163
 Conservative 100;
 Chong, Pele
 Loosmore,
 linear
 Sim & McBurney
 single
 4.6%; Score 172; DB 2; 1
21.4%; Pred. No. 6.9e-07;
1tive 100; Mismatches 291;
 Scott
 1038-410 MIS:jb
 Version
 Length 915;
 Indels 242;
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 APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Gray-overs, Anthony
APPLICANT: Gray-owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Mirchin, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
 E: Sim & McBurney
Suite 701, 330 University Avenue
 618 TGTHRTLSWNAGIVL---KPADWLDLTYR-----
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655 -EMYGWRSGDKIKAVKIDPEKSFNK 678
 670 DAMAAYRFTPKLK-LQINADNIFNR 693
 Sequence 96, Application US/08478373
Patent No. 5922841
 STREET: Suite 70
CITY: Toronto
STATE: Ontario
 GENERAL INFORMATION: APPLICANT: LOOSMO
 ADDRESSEE:
 RESULT 29
US-08-478-373-96
 COUNTRY:
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Best Local Similarity 21.4%; Pred. No. 6.9e-07;
Matches 172; Conservative 100; Mismatches 291; Indels 242;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER:
COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,373
FILING DATE: 07.0UN-1995
 NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg
TELECOMMUNICATION INFORMATION:
 CLASSIFICATION: 435

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APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY AGENT: INFORMATION:
NAME: STANSE NAME: STA
 (416) 595-1155
 TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 915 amino acids
 TYPE: amino acid
STRANDEDNESS: si
 linear
 TELEPHONE:
 US-08-478-373-96
 28
 265
 299
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Length 915; Indels 242;

Gaps

43;

57

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RESULT 30
US-08-474-671-96
 Sequence 96,
 GENERAL INFORMATION:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
 tent No.
 APPLICANT:
APPLICANT:
TITLE OF IN
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APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 TITLE OF INVENTION: Transferrin Receptor Genes
 FILING DATE: 08-NOV-1993 ATTORNEY/AGENT INFORMATION:
 FILING DATE: 29-DEC-1
PRIOR APPLICATION DATA:
 CORRESPONDENCE ADDRESS
 NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
 FILING DATE: 07
CLASSIFICATION:
 APPLICATION NUMBER: US 0 FILING DATE: 29-DEC-1993
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M5G 1R7
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 Suite 701, 330 University Avenue
 Gray-Owen, Scott
Yang, Yan-Ping
Murdin, Andrew
Klein, Michel
 Chong,
 Schryvers,
 Loosmore, Sheena
Harkness, Robin
 Sim & McBurney
 07-JUN-1995
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 Release #1.0,
 US 08/148,968
 Anthony
 US 08/175,116
 US/08/474,671
 Scott
 ---HKLLQAAFKKSFDTAKIRHNLSVNLGYDRFGSNLRHQD
 1038-465
 Version
 MIS:vg
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 -TSTGFRLPSFA--
 669
 895
 514
 654
 617
 ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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 RESULT 31
US-08-483-577A-96
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Sequence 96, Application US/08483577A
Patent NO. 6015688
GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena
APPLICANT: Harkness, Robin
 Matches 172;
 Query Match
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 Score 172; DB 3;]
Pred. No. 6.9e-07;
0; Mismatches 291;
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377

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159

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,438
 TITLE OF INVENTION: Transferrin Receptor Genes NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
DDDRESSEE: SIM & MCBUINEY
 E: Sim & McBurney
6th Floor, 330 University Avenue
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,577
FILING DATE: 07-UON-1995
PRIOR PRICKATION DATA:
APPLICATION NUMBER: US 08/337,483
 UMBER: US 08/337,483
08-NOV-1994
 DAMAAYRFTPKLK-LQINADNIFNR 693
 US-08-897-438-96
; Sequence 96, Application US/08897438
; Patent No. 6262016
 COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DX
 APPLICANT: LOOSMOZE, Sheena APPLICANT: Harkness, Robin APPLICANT: Schryvers, Anthony APPLICANT: Chong, Pele APPLICANT: Gray-Owen, Scott APPLICANT: Yang, Yan-Ping APPLICANT: Muzdin, Andrew APPLICANT: Klein, Michel
 FILING DATE:
CLASSIFICATION: 435
 Patent No. 6262016
GENERAL INFORMATION:
 Ontario
 STREET: 6th F
CITY: Toronto
 FILING DATE:
 STATE:
 430
 670
 477
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 43;
 :| : || : || GRIGGAEALLIRTGRHA------GEIRAHEAAGRG-VQSFNRLAPVDDGSKYAYFIVEE 262
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 3 QFMSVFRIN---MTAATVLAALSSSVFA--AQTADLETVHIKGQRSYNAIVTEKNGDYSS 57
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ilarity 21.4%; Pred. No. 6.9e-07;
Conservative 100; Mismatches 291; Indels 242;
 218 OTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYLYOORHLAPY----
 APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Gray-Owen, Scott
APPLICANT: Wandin, Andrew
APPLICANT: Windin, Andrew
APPLICANT: Klein, Michel
ITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSE: Sim.& McBurney
STREET: Suite 701, 330 Unviersity Avenue
CITY: Toronto
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATINE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
 CLASSIFICATION: 435
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
 AFFLING DATE: 07-JUN-1995
CLASSIFFORM:
 1038-511
 REFERENCE/DOCKET NUMBER: 1038
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEFAX: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 96: SEQUENCE CHARACTERISTICS: LENGTH: 915 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
Schryvers, Anthony
 24,973
 NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,
 SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Matches 172; Conservi
 linear
 COUNTRY: Canada
ZIP: M5G 1R7
 CITY: Toronto
STATE: Ontario
 US-08-483-577A-96
 265
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PRIOR APPLICATION DATA:

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 Matches 172;
 Query Match
 TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: (
 SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acid
 TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
 FILING DATE: 08-NOV-1993 ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
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 344
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 REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
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 FILING DATE:
 APPLICATION NUMBER:
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 Stewart, Michael
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 US 08/148,968
 US 08/175,116
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 1038-720
-- RWADVGAGLRYDYRSTHSDDGSVS
 Length 915;
 Indels
 242;
 Gaps
617
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 US-08-637-654-96
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 US-08-637-654-96
 Sequence 96, Application US/08637654 Patent No. 6358727
 Matches 172;
 Query Match
Best Local (
 TELEFAX: (416) 595-116
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 GENERAL INFORMATION:
APPLICANT: Loosmo
 REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,
 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
 APPLICANT:
 FILING DATE: 05-AUG-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
 MEDIUM TYPE: Floppy
 ADDRESSEE: Sim & McB
 HAEMOPHILUS TRANSFERRIN RECEPTOR GENES NUMBER OF SEQUENCES: 147
 APPLICANT:
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TOPOLOGY: 111
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M5G 1R7
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Gray-Owen, Scott
Yang, Yan-Ping
 6th Floor, 330 University Avenue
 Murdin, Andrew D
Klein, Michel H
 Conservative 100;
 Loosmore, Sheena !
Harkness, Robin E
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 linear
 Sim & McBurney
 05-AUG-1996
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 4.6%; Score 172; DB 4;
21.4%; Pred. No. 6.9e-07;
 US/08/637,654
 Anthony
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 PCT/CA94/00616
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 1038-595
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 Mismatches
 Version
 Length 915;
 Indels 242;
 Gaps
 57
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 APPLICANT: LOOSMOZE, Sheena
APPLICANT: Barkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Gray-Owen, Scott
APPLICANT: Windin, Andrew
APPLICANT: Klein, Michel
ITILE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEGUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurner:
STREET: 6th Flor
 COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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 - EMYGWRSGDKIKAVKIDPEKSFNK 678
 DAMAAYRFTPKLK-LQINADNIFNR 693
 CITY: Toronto
STATE: Ontario
 US-08-649-518-96
 299
 457
 563
 670
 218
 265
 402
 344
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 263 ECKNG----GHEKCKANPKKDVVGEDKRQTVSTRDYTGPNRFLADPLSYESRSWLFRPGF 318
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 402 RTTLYARGGLAL-NEFRSIPQVDLIANARKGVRGYSHTVATENLDEFG----IYGKSTFH 456
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 ----TGYAGAVYDLNDNN 504
 58 FAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA 117
 Gapa
 2 QOQHLFRLNILCLSLMTALPAYAENVQAQQAQEKQLDTIQVKAKKQKTRRDNEVTG---- 57
 3 QFMSVFRIN---MTAATVLAALSSSVFA--AQTADLETVHIKGQRSYNAIVTEKNGDYSS
 218 QTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPY------
 -PADLKHYFGNGGYGKVGMRYSDRDA------DSNYAFAGSKLGMKTPAGR---P
 344 GCNTADDKACAVG--LGTEIKOKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEOG
 | : : | | : | | | 378 GLFTSGENNAPVGAEYGTGVFYDETHTKSRYGLEYVYTNADKD--TWADYARLS-----
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 Query Match
4.6%; Score 172; DB 4; Length 915;
Best Local Similarity 21.4%; Pred. No. 6.9e-07;
Matches 172; Conservative 100; Mismatches 291; Indels 242;
 457 PADGLSLIGGGRLGHYKIESGEGKTLHKASKTKF----
 PRIOR AND DATE:

APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-608
TELECOMMUNICATION: INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,518
FILING DATE: 17-MAY-1996
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,577
 TELEPHONE: (416) 595-1155
 FILING DATE: 07-JUN-1995
 LENGTH: 915 amino acids
TYPE: amino acid
STRANDEDNESS: single
 TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 linear
 US-08-649-518-96
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| Query Match 4.5%; Score 171; DB 2; Length 909; Best Local Similarity 18.2%; Pred. No. 8.4e-07; Matches 180; Conservative 128; Mismatches 327; Indels 356; Gaps 49; | amino acid<br>Y: linear<br>TYPE: prote | ; TELEFAX: (212) 645-2054 ; INFORMATION FOR SEQ ID NO: 4: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 909 amino acids | ; REGISTRATION NUMBER: 37,066 ; REFERENCE/DOCKET NUMBER: SPA-1-PDC ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (212) 645-1405 | ; APPLICATION NUMBER: US 07/572,187 ; FILING DATE: 23-AUG-1990 ; ATTORNEY/AGENT INFORMATION: ; NAME: Gallagher, Thomas C. | ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 07/973,336 ; FILING DATE: 05-NOV-1992 ; PRIOR APPLICATION DATA: | ; CLASSIFICATION: 536 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/124,254 ; FILING DATE: 20-SEP-1993 | ; SOFTWARE: PatentIn Release #1.0, Version #1.25; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/363,124A ; FILING DATE: 23-DEC-1994 | 299                                                                 | CITY: New York  STATE: New York  COUNTRY: USA  ZIP: 10014               | )EQUENCES: 8  NCE ADDRESS: IMClone Systems Incorporated 180 Varick Street | APPLICANT: Sparling, P. Frederick APPLICANT: Cornelissen, Cynthia N. TITLE OF INVENTION: Transferrin-Binding Proteins From TITLE OF INVENTION: Neisseria Conorrhea and Neisseria Meningitidis | H 3 0 W                                   | Db 655 -EMYGWRSGDKIKAVKIDPEKSPNK 678       | 670 DAMAAYRFTPKLK-LOINADNIFNR 693                              | QY 613 TASNSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATF 669   :- | 569 YTDCTPRSINGKSYYAAVRDNVRLGRWADVGAGLRYDYRSTHSDDGSVS | Db 515 YYYQSANRAYSLKTPPQNNGKKTSPNGREKNPYWYSIGRGNVVTRQICLFGNNT 568  Oy 563 AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKW-QIHAGYSYLHSOIK 612 | Db 477                                                        |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------|-----------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------|-------------------------------------------------------------------------|---------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------|--------------------------------------------|----------------------------------------------------------------|---------------------------------------------------------------------------|-------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------|
| RESULT 36<br>US-08-817-707-8<br>; Sequence 8, Application US/08817707<br>; Patent No. 6277382                                                                      | Qy 696YARVGGANTENIPGSERTWTANLRY 720 :  | Qy 646 GGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTFKLKLQINADNIFNRHY 695                                                   | Qy 615 SNSRDDGIFLLMPKHSANLWTTYQVTPBLTI 645                                                                                      | Qy 564 APLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTA 614                                                            | Qy 519 NLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSF-YRMKDKNAA 563                                                          | Qy 480KTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQT 518                                                              | Qy 433 RGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRIGHYKIESGEG 479 :  :  :  :  :  :  :        :  :                                                  | Qy 377 RLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGV 432 | Qy 317 RYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPF 376 | Qy 257 QQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGM 316   | Qy 234 ETFYAAADWDINP                                                                                                                                                                          | Qy 204 SLNSDGSVRGRVMAQTVGASPRPABKNNRH 233 | OY 172LVRKRETKAFQGHAAAGFGTHKQYKAEADVSG 203 | 8 NSSEYGNGALAGSVAFQTKTAADIIGEGKQWGIQSKTAYSGKDHALTQSLALAGRSGGAE | 99                                                                        | 116                                                   | Qy 56 SSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSV 115                                                            | Qy 3 QFMSVFRINWTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDY 55 |

```
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
 ; Sequence 16, Application US/08613009A; Patent No. 6090576
 TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
 908 amino acids
 APPLICANT: Myers, Lisa E
 ----- 809 HSQ-----
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 3: Ontario
FRY: Canada
M5G 1R7
 ; TOPOLOGY: linear
US-08-613-009A-16
 TYPE: amino acid
STRANDEDNESS: si
 GENERAL INFORMATION:
 US-08-613-009A-16
 COUNTRY:
 LENGTH:
 원
 8
 g
 8
 31;
 170 LLLDDRQFGVMMKNGYSSRNREWTNTLGFGVSNDRVDAALLYSQRRGHETESAGERGYPV 229
 126 NSSRLSIDPELVR------OTLQCHD 169
 DGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRH----- 260
 : | : : : | | | : : : | | 230 EGAGSGAIIRGSSRGIPDPSK--HKYHNFLGKIAYQINDKHRIGPSFNGQQGHNYTIEES 287
 --LAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHY-----FGNGG-- 310
 288 YNLTASSWREADDVNR----RRNANLFYEWTPDSNWLSSLKADFDYQTTKVAAVNNKGSF 343
 73 IPOSVSIITNOOVKDRNVDTFDQLARKTPGLRVLSNDDG-----RSSVYARGYEYSEY 125
 69 NKDLVRYSTDVGLSDSGRHOKGFAVRGVEGNRVGVSIDGVSLPDSEENSLYAR---YGNF 125
 126 NIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGH- 184
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 ---YGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALA 367
 FDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIAN 427
 18 LAALSSSVF----AAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLRE 72
 9 IAALVGSIFGNPVLAADBAATETTPVKAEIKEVRVKDQLNAPATVERVNLGRIQQEMIRD 68
 APPLICANT: Hwa, Vivian
APPLICANT: Heffron, Fred
APPLICANT: Heffron, Xavier
TITLE OF INVENTION: No. 6277382el Bacterial Hemoglobin Receptor
TITLE OF INVENTION: Genes and Uses
NUMBER OF SEQUENCES: 15
 Query Match
4.5%; Score 169.5; DB 4; Length 790;
Best Local Similarity 18.5%; Pred. No. 9.2e-07;
Matches 153; Conservative 102; Mismatches 336; Indels 235;
 OPERATION SYSTEM: PC-DOS/MG-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/817,707
FILING DATE: 19-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6277382nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 94,784-J
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 312-913-0001
 ADDRESSEB: McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive, 32nd Floor CITY: Chicago STATE: Illinois COUNTRY: USA
 ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
 PTDYSTWTRNYNOKDLENIY---
 : 790 amino acids amino acid
 TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-817-707-8
 CORRESPONDENCE ADDRESS
GENERAL INFORMATION:
 APPLICANT:
APPLICANT:
APPLICANT:
 LENGTH:
 368
 311
 185
 208
 344
 261
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378 MD---SQPLQLG------GRHRLSLKTFASRREFENLNRDDYYFS 413
 485 ASKTK-----FTGYAGAVYDLN-----DNNSLYL--SLSQLY-----TPQ 517
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 643 KSKLSGDNSLLSTQPPKVIAGİDYESPSEKWGVFSRLTYLGAKKAKDAQYTVYENKGRĞT 702
 APPLICANT: Schryvers, Anthony B
APPLICANT: Barkness, Robin B
APPLICANT: Harkness, Robin B
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
CORRESPONDENCE: 31
CORRESPONDENCE ADDRESS:
 650 NAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY 695
 703 PLOKKVKDYPWLNKSAY-VFDMYGFYKLAKNLTLRAGVYNVFNRKY 747
 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/613,009A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 1038-542
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
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 Query Match
4.5%; Score 169.5; DB 3; Length 908;
Best Local Similarity 18.0%; Pred. No. 1.2e-06;
Matches 177; Conservative 125; Mismatches 341; Indels 339; Gaps
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 157 SGLFDSSGEMGGIVN-----
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 RLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYS
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 QQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGM 316
 KLKEDASVKDERKTVSTÓDYTGŚNŔLLANPLEYGSQSWLFRPGWHLDŃŔĤYVGAVLERTQ
 .---- 171
 722
 543
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 396
 337
 98
 770
 436
 46;
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|    | Qy 204 SLNSDGSVRGRVMAQTVGASPRPAEKNNRH 233                                                                                                                                    | D D       |  |
|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------|--|
|    | Qy 172LVRKRPTKAFQGHAAAGFGTHKQYKAEADVSG 203<br>                                                                                                                               | ס ט       |  |
|    | Qy 157 SGLFDSSGEMGGIVN                                                                                                                                                       | .`<br>ຫຼ  |  |
|    | Qy 116 YA-RGYEYSBYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGP 156                                                                                                                        | 4d<br>40  |  |
|    | Qy 56 SSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSV 115                                                                                                       | ם ט       |  |
|    | Qy 3 QFMSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDY 55                                                                                                                | ס ט       |  |
| 46 | Query Match 4.5%; Score 169.5; DB 4; Length 908; Best Local Similarity 18.0%; Pred. No. 1.2e-06; Matches 177; Conservative 125; Mismatches 341; Indels 339; Gaps             |           |  |
|    | ME MA                                                                                                                                                                        | <b>G</b>  |  |
|    | NAME: STEWART, MICHAEL I  REGISTRATION NUMBER: 24973  REFERENCE/DOCKET NUMBER: 1038-664  TELECOMMUNICATION INFORMATION:  TELEPHONE: (416) 595-1163  TELEPHAX: (416) 595-1163 |           |  |
|    | CATION NUME G DATE: 03 IFICATION: Y/AGENT INI                                                                                                                                |           |  |
|    | MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: PatentIn Release #1.0, Version #1.30  CURRENT APPLICATION DATA:            |           |  |
|    | 1225                                                                                                                                                                         |           |  |
|    | CORRESONDENCE ADDRESS: ADDRESSEE: Sim & McBurney STREET: 6th Floor, 330 University Avenue CITY: Toronto                                                                      |           |  |
|    | APPLICANT: Yang, Yan-Ping APPLICANT: Yang, Yan-Ping APPLICANT: Klein, Michel H TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella NIMBER OF SCOTENCES. 43           |           |  |
|    | Schryvers, A<br>Harkness, Ro<br>Loosmore, Sh                                                                                                                                 |           |  |
|    | Sequence 22, Application US/08//85/08 Patent No. 6437096 GENERAL INFORMATION: APPLICANT: Myers, Lisa E                                                                       | · · · · · |  |
|    | ĩ                                                                                                                                                                            | · C 75    |  |

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544 IGKTTVNTSPICRFGNNTYTDCTPRNIGGNGYYAAVQDNVRLGRW-ADVGAGIRYDYRST 602
 623
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 L------LMPK------HSANLW----TTYQ-----VTPELTIGGGVNAMSG 654
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 655 ITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY-------YAR 698
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 KTRYAA----LGKRVMEGVETEISGAVTPKW-----QIHAGYSYLHSQIKTASNSRDDGIF
 APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin B
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Min-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Wichel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 60
 ZIP: MSG 1K,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: Release #1.0, Version #1.30
 STATE: Ontario
COMPRY: Canada
ZIP: MSG 1R7
COUNTRY: Canada
ZIP: MSG 1R7
COMPRY: Canada
 Sequence 22, Application US/09059584
Patent No. 6440701
 VGGANTFNI PGSERTWTANLRY 720
 GENERAL INFORMATION:
APPLICANT: Myers, Lisa E
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCE
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56 SSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSV 115
 116 YA-RGYEYSEYN--IDGLPAQMQS-----INGTLP-----NLFAFDR---VEVMRGP 156
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 544 IGKTTVNTSPICRFGNNTYTDCTPRNIGGNGYYAAVQDNVRLGRW-ADVGAGIRYDYRST 602
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 Gaps
 3 QFMSVFRINMTAATVLAALSSSVFA-----AQTADLETVHIKGQRSYNAIVTEKNGDY 55
 DTAKIRHNLSINLGYDRFKS--QLSHSDYYLQNAVQAYDLITPPKPPFPNGSKDNPYRVS
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 Indels 339;
 Query Match
4.5%; Score 169.5; DB 4;
Best Local Similarity 18.0%; Pred. No. 1.2e-06;
Matches 177; Conservative 125; Mismatches 341;
 APPLICATION NUMBER: US 08/778,570
FILING DATE: 03-JAN-1997
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-794
TELECOMMUNICATION INFORMATION:
 ---LVRKRPTKAFQGHAAAGFGTH----
 ETF----YAAADWDINP---
 TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEC ID NO: 22:
SEQUENCE CHARACTERISTICS:
14-APR-1998
 LENGTH: 908 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
 TOPOLOGY:
US-09-059-584-22
 157
 158
 172
 234
 397
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|                                    |                                                                  |                                                           |                                                                      |                                         |                                                           |                                                              |                                                                      |                                                        |                                                                      |                                                |                                                                      |           |                                                            |   |                                                               |                                                                      |                                              |                                                                      |                                                                      |                   |                                                                      |                                        |                                                                      |                          |    |                         |                                                                     |                      |                                                | •                                                                   |                                                               |                                                            |                                                                                                                                                                      |
|------------------------------------|------------------------------------------------------------------|-----------------------------------------------------------|----------------------------------------------------------------------|-----------------------------------------|-----------------------------------------------------------|--------------------------------------------------------------|----------------------------------------------------------------------|--------------------------------------------------------|----------------------------------------------------------------------|------------------------------------------------|----------------------------------------------------------------------|-----------|------------------------------------------------------------|---|---------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|-------------------|----------------------------------------------------------------------|----------------------------------------|----------------------------------------------------------------------|--------------------------|----|-------------------------|---------------------------------------------------------------------|----------------------|------------------------------------------------|---------------------------------------------------------------------|---------------------------------------------------------------|------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| B 8                                | Db                                                               | Ş                                                         | Db                                                                   | Ş                                       | Дb                                                        | ş                                                            | 망                                                                    | 8,                                                     | Db                                                                   | Ş                                              | 뮹                                                                    | Ş         | 망                                                          | Ş | B                                                             | Ş                                                                    | 뮹                                            | Ş                                                                    | 뮍                                                                    | Ş                 | Дb                                                                   | Ş                                      | Дb                                                                   | Ş                        | Db | Ş                       | 망                                                                   | Ş                    | 당                                              | Ş                                                                   | 뮹                                                             | Ş                                                          | Qu<br>Be<br>Mai                                                                                                                                                      |
| 696YARVGGANTFNIPGSERTWTANLRY 720 : | 823 GNANAKKAASRRTRPWYVTDVSGYYNIKKHLTLRAGVYNLLNYRYVTWENVRQTAG 878 | 647 GGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY 695 | 763 DIRADRTFVTSYLFDAVQPSRYVLGLGYDHPDGIWGINTMFTYSKAKSVDELLGSQALLN 822 | 616 NSRDDGIFLLMPKHSANLWTTYQVTPELTIG 646 | 715 DPGYRNAQNARIAGINILGKIDWHGVWGGLPDGLYSTLAYNRIKVKDA- 762 | 564 APLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTAS 615 | 655 GESLKTLDLKPEKSFNREAGIVFKGDFGNLEASYFNNAYRDLIAFGYETRTQNGQTSASG 714 | 519 NLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSF-YRMKDKNAA 563 | 595 IRYDYRSTHSEDKSVSTGTHRNLSWNAGVVLKPFTWMDLTYRASTGFRLPSFAEMYGWRA 654 | 480KTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQT 518 | 536 KDNPYRVSIGKTTVNTSPICRFGNNTYTDCTPRNIGGNGYYAAVQDNVRLGRW-ADVGAG 594 | TFHPADGLS | 486 DTAKIRHNLSINLGYDRFKSQLSHSDYYLQNAVQAYDLITFKKPPFPNGS 535 | z | 433 DLDNRLQQTHCSHDGSDKNCRPDGNKPYSFYKSDRMIYEESRNLFQAVFKKAF 485 | 317 RYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPF 376 | 397 DERHTKNRYGVEYVYHNADKDTWADYARLSYDRQGI 432 | 257 QQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKWNSHDVFADLKHYFGNGGYGKVGM 316 | 338 QTFDTRDMTVPAYFTSE-DYVPGSLKGLGKYSGDNKAERLFVQGEGSTLQGIGYGTGVFY 396 | 234 ETFYAAADWDINP | 278 KLKEDASVKDERKTVSTQDYTGSNRLLANPLEYGSQSWLFRPGWHLDNRHYVGAVLERTQ 337 | 204 SLNSDGSVRGRVMAQTVGASPRPAEKNNRH 233 | 218 ALLIYTKRRGREIHAHKDAGKGVQSFNRLVLDEDKKEGGSQYRYFIVEEECHNGYAACKN 277 | 172LVRKRPTKAFQGHAAAGFGTH | :  | 157 SGLFDSSGEMGGIVN 171 | 99 YSIRGMDKNRVSLTVDGV-SQIQSYTAQAALGGTRTAGSSGAINEIEYENVKAVEISKGS 157 | AQMQSINGTLPNLFAFDRVE | 58LGKLVKSSDTLSKEQVLNIRDLTRYDPGIAVVEQGRGASSG 98 | 56 SSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSV 115 | 2 QQQHLFRLNILCLSLMTALPVYAENVQAEQAQEKQLDTIQVKAKKQKTRRDNEVTG 57 | 3 QFMSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDY 55 | Query Match 4.4%; Score 167.5; DB 1; Length 908; Best Local Similarity 18.2%; Pred. No. 1.8e-06; Matches 180; Conservative 125; Mismatches 330; Indels 355; Gaps 49; |

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APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Wide, Yan-Ping
APPLICANT: Michel
TITLE OF INVENTION: Transferrin Receptor Genes
CORRESPONDENCE ADDRESS:
 696 ----YARVGGANTFNIPGSERTWTANLRY 720
 879 GAVNOHKNVGVYNRYAAPGRNYTFSLEMKF 908
 ---LVRKRPTKAFQGHAAAGFGTH----
 Sequence 94, Application US/08337483; Patent No. 5922562; GENERAL INFORMATION:
 Loosmore, Sheena
Harkness, Robin
Schryvers, Anthony
 ADDRESSEE: Sim & McBurney
 APPLICANT:
APPLICANT:
 US-08-337-483-94
 APPLICANT:
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 49;
 56 SSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSV 115
 116 YA-RGYEYSEYN--IDGLPAQMQS-----INGTLP-----NLFAFDR---VEVMRGP 156
 ----- 171
 58 ------LGKLVKSSDTLSKEQVLN----IRDLTRYDPGIAVVEQGRGASSG 98
 2 QOQHLFRINILCLSIMTAL -- PVYAENVQAEQAĞEKQLDTIQVKAKKQKTRRDNEVTG -- 57
 3 QFMSVFRINMTAATVLAALSSSVFA-----AQTADLETVHIKGQRSYNAIVTEKNGDY 55
 Query Match
4.4%; Score 167.5; DB 2; Length 908;
Best Local Similarity 18.2%; Pred. No. 1.8e-06;
Matches 180; Conservative 125; Mismatches 330; Indels 355;
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,435
 APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
 1038-462 MIS:vg
 FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
 FILING DAIE: ... 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
 UMBER: US/08/478,435
07-JUN-1995
 Sequence 94, Application US/08478435 Patent No. 5922323
 Loosmore, Sheena
Harkness, Robin
Schryvers, Anthony
 NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
 REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
 TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acids
 (416) 595-1155
 157 SGLFDSSGEMGGIVN----
 ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 TYPE: amino acid
STRANDEDNESS: Bi
 Ontario
: Canada
 CITY: Toronto
STATE: Ontario
COUNTRY: Canada
 TELEPHONE:
 US-08-478-435-94
 US-08-478-435-94
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234 ETF-----YAAADWDINP----LY 256 257 QQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGM 316 317 RYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPF 376 433 DLDNRLQQTHCSHDGSDKNCRPDGNKPYSFYKSDRMI-----YEESRNLFQAVFKKAF 485 377 RLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANAR----KGV 432 486 DTAKIRHNLSINLGYDRFKS--QLSHSDYYLQ-----NAVQAYDLITPKKPPFPNGS 535 433 RGYSHTVA----TENLDEFGIYGKSTFHPADGLSLIGGG-----RLGHYKIESGEG 479 :: | | :: | | :: | | 595 IRYDYRSTHSEDKSVSTGTRNLSWNAGVVLKPFTWMDLTYRASTGFRLPSFAEMYGWRA 654 655 GESLKTLDLKPEKSFNREAGIVFKGDFGNLEASYFNNAYRDLIAFGYETRTONGQTSASG 714 564 APLNPNNKKTRYAA---LGKRVMEGVETEISGAVTPKW----QIHAGYSYLHSQIKTAS 615 715 DPGYRNAQNARIAGINILGKIDWHGV------WGGLPDGLYSTLAYNRIKVKDA- 762 616 NSRDDGIFL-----VTPELTIG 646 763 DIRADRIFVISYLFDAVQPSRYVLGLGYDHPDGIWGINTMFTYSKAKSVDELLGSQALLN 822 ------KQYK------AEADVSG 203 218 ALLIYTKRRGREIHAHKDAGKGVQSFNRLVLDEDKKEGGSQYRYFIVEEECHNGYAACKN 277 397 DERHIKORRYGV------EYVYHNAD-----KDTWAD----YARLSYDRQGI 432 823 GNANA----KKAASRRTRPWYVTDVSGYYNIKKHLTLRAGVYNLLNYRYVTWENVRQTAG 878 204 SLNSDGSV---RGRVMAQTVGASPR----PAE------KONRH---------KTLHKASKTKFTG-----YAGAV-----YDLNDNNSLYL---SLSQLYTPQT 519 NLDADGKLLKPRQGNQFEVG--YKG-----SYMDDRLNARVSF-YRMKDKN----AA 647 GGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY------

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
STRANDEDNESS: single
; TOPOLOGY: linear
US-08-337-483-94
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 Query Match 4.4%; Score 167.5; DB 2; Length 908; Best Local Similarity 18.2%; Pred. No. 1.8e-06; Matches 180; Conservative 125; Mismatches 330; Indels 355; Gaps
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 94:
 APPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUREENT APPLICATION DATA:
ARBITCATION NUMBER. 17/08/227 462
 COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 338
486 DTAKIRHNLSINLGYDRFKS--QLSHSDYYLQ-----NAVQAYDLITPKKPPFPNGS 535
 397
 257
 278
 204 SLNSDGSV---RGRVMAQTVGASPR----PAE------KUNRH------ 233
 218
 158
 157
 116 YA-RGYEYSEYN--IDGLPAQMOS-----INGTLP-----NLFAFDR----VEVMRGP 156
 99
 56
 58 -----İGKLVKSSDTLSKEQVLN----IRDLTRYDPĞIAVVEQGRGASSG 98
 N
 w
 SSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSV 115
 QFMSVFRINMTAATVLAALSSSVFA-----AQTADLETVHIKGQRSYNAIVTEKNGDY 55
 RYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPF 376
 DERHTKNRYGV------EYVYHNAD------KDTWAD----YARLSYDRQGI 432
 QTFDTRDMTVPAYFTSE-DYVPGSLKGLGKYSGDNKAERLFVQGEGSTLQGIGYGTGVFY 396
 ---LVRKRPTKAFQGHAAAGFGTH-------KQYK-----AEADVSG 203
 RLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANAR----KGV 432
 DLDNRLQQTHCSHDGSDKNCRPDGNKPYSFYKSDRMI ---
 QQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGM 316
 ETF-----YAAADWDINP----LY 256
 KLKEDASVKDERKTVSTODYTGSNRLLANPLEYGSQSWLFRPGWHLDNRHYVGAVLERTQ 337
 ALLIYTKRRGREIHAHKDAGKGVOSFNRLVLDEDKKEGGSOYRYFIVEEECHNGYAACKN 277
 NSSEYGNGALAGSVAFQTKTAADIIGEGKQWGIQSKTAYSGKDHALTQSLALAGRSGGAE 217
 SGLFDSSGEMGGIVN------
 YSIRGMDKNRVSLTVDGV-SQIQSYTAQAALGGTRTAGSSGAINEIEYENVKAVEISKGS 157
 QQQHLFRLNILCLSLMTAL--PVYAENVQAEQAQEKQLDTIQVKAKKQKTRRDNEVTG-- 57
 Toronto
 Ontario
 Suite 701,
 330 Unviersity Avenue
 ----- 171
 ----YEESRNLFQAVFKKAF 485
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| TRATION NIMBER: 24                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |             |  |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------|--|
| NAME: Stewart Michael I                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |             |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ٠.,         |  |
| ATION NU                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ٠.          |  |
| PRIOR APPLICATION DATA:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | •• •        |  |
| FILING DATE: 29-DEC-1993                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |             |  |
| A:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | . ••        |  |
| SSIFICATION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ٠.          |  |
| NG DATE: 08-NOV-1994                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |             |  |
| APPLICATION NUMBER: US 08/337,483                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |             |  |
| PRIOR APPLICATION DATA:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |             |  |
| `                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |             |  |
| NUMBER: US/                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | . <b></b>   |  |
| CATION DATA:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ٠.          |  |
| ARE: Pat                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ٠.          |  |
| SYSTEM: PC-DOS/MS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | •••         |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |             |  |
| TYPE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ~           |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | . •.        |  |
| IRY:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |             |  |
| 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ٠.          |  |
| Toronto                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ٠.          |  |
| uite 701                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |             |  |
| MCBurno                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |             |  |
| CODDECONTENCE ADDECC. 147                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |             |  |
| Tra                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ٠.          |  |
| Klein, Michel                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ٠.          |  |
| : Murdin                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | <b>~.</b> · |  |
| : Yang, Yan-P                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |             |  |
| APPLICANT: Grav-Owen. Scott                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | •           |  |
| α                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | . ~.        |  |
| Harkness, k                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |             |  |
| CANT: Loosmore,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ٠.          |  |
| AL INFORM                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |             |  |
| 5922841                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |             |  |
| 373-94                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | . su        |  |
| SULT 43                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | RESU        |  |
| 879 GAVNOHKNÝGVYNRYAAPGRNYTESLEMKE 908                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Db          |  |
| 696YARVGGANTENIPGSERTWTANLRY 720                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | δ           |  |
| 823 GNANAKKAASKKIKPWIYIUVSGIINLKKHLILKAGVINLLNIKIVIWENVKQIAG 87                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | מע          |  |
| :-<br>:-<br>:-<br>:-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ! !         |  |
| 647 GGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLOINADNIFNRHY 69                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Ş           |  |
| 763 DIRADRTFVTSYLFDAVQPSRYVLGLGYDHPDGIWGINTMFTYSKAKSVDBLLGSQALLN 82                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ర్జ         |  |
| 616 NSRDDGIFLLMPKHSANLWTTYQVTPELTIG 64                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Ş           |  |
| 715 DÞGYRNAQNARÍAGINILGKIDWHGVWGGLPDGLYSTLAYNRIKVKDÁ- 76                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ממ          |  |
| 564 APLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTAS 61                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | δ           |  |
| 655 GESLKTLDLKPEKSFNREAGIVFKGDFGNLEASYFNNAYRDLIAFGYETRTQNGQTSASG 71                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Дb          |  |
| 519 NUUAUGRULKERQGNQEEVG1KGSIMUUKLNAKVSE-IKMKUKNAA 56                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Ş           |  |
| ייי דאינים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מסנים אין מ | ?           |  |
| 595 IRYDYRSTHSEDKSVSTGTHRNLSWNAGVVLKPFTWMDLTYRASTGFRLPSFAEMYGWRA 65                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Db          |  |
| 480KTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQT 51                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ş           |  |
| 536 KDNPYRVSIGKTTVNTSPICRFGNNTYTDCTPRNIGGNGYYAAVQDNVRLGRW-ADVGAG 59                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Db          |  |
| TFHPADGLSLIGGGRLGH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Ş           |  |

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| | | | : | | : | : | DIRADRIFVTSYLFDAVQPSRYVLGLGYDHPDGIWGINTMFTYSKAKSVDELLGSQALLN 822
 3 QFMSVFRINMTAATVLAALSSSVFA-----AQTADLETVHIKGQRSYNAIVTEKNGDY
 SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
 Query Match
4.4%; Score 167.5; DB 3;
Best Local Similarity 18.2%; Pred. No. 1.8e-06;
Matches 180; Conservative 125; Mismatches 330;
 3: Sim & McBurney
Suite 701, 330 University Avenue
 1038-465 MIS:vg
 ----YARVGGANTFNIPGSERTWTANLRY 720
 879 GAVNQHKNVGVYNRYAAPGRNYTFSLEMKF 908
 PAPLICATION NUMBER: US/08/474,671
FILING DATE: 07-JUN-1995
CLASSIPICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
FILING DATE: 29-DEC-1993
 US 08/148,968
 ; Sequence 94, Application US/08474671; Patent No. 6008326
 ...ppy disk
Compatible OPERATING SYSTEM: PC-DOS'
 NAME: Stewart, Michael I
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 94
 Loosmore, Sheena
Harkness, Robin
 FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
 908 amino acids
 ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
 CURRENT APPLICATION DATA
 SEQUENCE CHARACTERISTICS
 APPLICATION NUMBER:
 TYPE: amino acid
STRANDEDNESS: siz
 linear
 GENERAL INFORMATION:
APPLICANT: LOOSMO
 STREET: Suite
CITY: Toronto
 ADDRESSEE:
 US-08-474-671-94
 LENGTH:
 763
 969
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 :| :: | | :: | | :: | | 33 DLDNRLQQTHCSHDGSDKNCRPDGNKPYSFYKSDRMI-----YEESRNLFQAVFKKAF 485
 DTAKIRHNLSINLGYDRFKS--QLSHSDYYLQ-----NAVQAYDLITPKKPPFPNGS 535
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 278 KLKEDASVKDERKTVSTQDYTGSNRLLANPLEYGSQSWLFRPGWHLDNRHYVGAVLERTQ 337
 ---DTVLGAGY----LY 256
 QORHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGM 316
 RYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKOKALAFDASYSRPF 376
 377 RLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANAR----KGV 432
 ----KTLHKASKTKFTG-----YAGAV-----YDLNDNNSLYL---SLSQLYTPQT 518
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 564 APLNPNNKKTRYAA---LGKRVMEGVETEISGAVTPKW-----QIHAGYSYLHSQIKTAS 615
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 YA-RGYEYSEYN--IDGLPAQMQS----INGTLP-----NLFAFDR---VEVMRGP 156
 218 ALLIYTKRRGREIHAHKDAGKGVQSFNRLVLDEDKKEGGSQYRYFIVEEECHNGYAACKN 277
 ------EYVYHNAD-----KDTWAD----YARLSYDRQGI 432
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 Gaps
 2 QQQHLFRLNILCLSLMTAL--PVYAENVQAEQAQEKQLDTIQVKAKKQKTRRDNEVTG-- 57
 58 -----LGKLVKSSDTLSKEÖVLN----IRDLTRYDPGIAVVEQGRGASSG 98
 3 QFMSVFRINMTAATVLAALSSSVFA-----AQTADLETVHIKGQRSYNAIVTEKNGDY
 204 SLNSDGSV---RGRVMAQTVGASPR----PAE-------KNNRH-----
 RGYSHTVA----TENLDEFGIYGKSTFHPADGLSLIGGG-----RLGHYKIESGEG
 DPGYRNAQNARIAGINILGKIDWHGV-------WGGLPDGLYSTLAYNRIKVKDA-
 Best Local Similarity 18.2%; Pred. No. 1.8e-06;
Matches 180; Conservative 125; Mismatches 330; Indels 355;
 Length 908;
 DB 2;
 4.4%; Score 167.5; DB 2
18.2%; Pred. No. 1.8e-06;
REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
 ETF-----YAAADWDINP-
 ; TOPOLOGY: linear
US-08-478-373-94
 397 DERHTKNRYGV---
 Query Match
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49; 823 GNANA----KKAASRRTRPWYVTDVSGYYNIKKHLTLRAGVYNLLNYRYVTWENVRQTAG 878 647 GGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY-----Length 908; APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Murdin, Andrew
APPLICANT: Murdin, Andrew
APPLICANT: Murdin, Andrew
APPLICANT: Murdin, Andrew
APPLICANT: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:

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RESULT 45
US-08-483-577A-94
; Sequence 94, Application US/08483577A
; Patent No. 6015688
; GENERAL INFORMATION:
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 317 RYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPF 376
 257
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 56
 N
 DPGYRNAQNARIAGINILGKIDWHGV-------WGGLPDGLYSTLAYNRIKVKDA- 762
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 APLNPNNKKTRYAA---LGKRVMEGVETEISGAVTPKW----QIHAGYSYLHSQIKTAS 615
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 DTAKIRHNLSINLGYDRFKS--QLSHSDYYLQ-----NAVQAYDLITPKKPPFPNGS
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 NSSEYGNGALAGSVAFQTKTAADIIGEGKQWGIQSKTAYSGKDHALTQSLALAGRSGGAE
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 ---LVRKRPTKAFQGHAAAGFGTH-------KQYK-----AEADVSG
 646
 479
 396
 256
 203
 217
 171
 57
 695
 714
 594
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 8
 US-08-483-577A-94
 Matches 180;
 Query Match
Best Local Similarity
 APPLICATION NUMBER: US/08/483,577A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael 1
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-511
 TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
 APPLICANT:
APPLICANT:
APPLICANT:
 ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 APPLICANT:
APPLICANT:
APPLICANT:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
 SEQUENCE CHARACTERISTICS:
 TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
 APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
 CORRESPONDENCE ADDRESS:
 APPLICANT:
 172
 158
 116
218 ALLIYTKRRGREIHAHKDAGKGVQSFNRLVLDEDKKEGGSQYRYFIVEEECHNGYAACKN
 58
 STRANDEDNESS:
TOPOLOGY: li
 CITY: Toronto
 56
 COUNTRY:
 ADDRESSEE: Sim & McBurney
 ω
 N
 QFMSVFRINMTAATVLAALSSSVFA-----AQTADLETVHIKGQRSYNAIVTEKNGDY 55
 ---LVRKRPTKAFQGHAAAGFGTH-------KQYK-----AEADVSG
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 QQQHLFRLNILCLSLMTAL--PVYAENVQAEQAQEKQLDTIQVKAKKQKTRRDNEVTG-- 57
 MSG 1R7
 amino acid
 Ontario
 908 amino acids
 Suite 701, 330
 4.4%; Score 167.5; DB 3; ilarity 18.2%; Pred. No. 1.8e-06; Conservative 125; Mismatches 330;
 Murdin, Andrew
Klein, Michel
 Gray-Owen, Scott
Yang, Yan-Ping
 Chong,
 Schryvers,
 Loosmore, Sheena
Harkness, Robin
 linear
 Floppy disk
 single
 Pele
 ĹGKĽVKŚSDTĽSKEQVĽN----IRDĽTŘYDPGIAVVEQGRĜASSG
 Anthony
 US/08/483,577A
 Unviersity Avenue
 Version
 #1.25
 Length 908;
 Gaps
 157
 203
 217
 171
 98
277
 49;
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Search completed: December 18, 2002, 06:47:00 Job time : 28.862 secs

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OM protein -
protein search, using
 Copyright
 GenCore version 5.1.3
(c) 1993 - 2002 Compugen Ltd
 sw model
```

Run December 18, 2002, 06:40:34 ; Search time 27.0814 Seconds (without alignments) 2562.980 Million cell updates/sec

Title: Perfect score: US-09-889-267-2 3776

MGQFMSVFRINMTAATVLAA......NTFNIPGSERTWTANLRYSF 722

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum Maximum DB BB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 10 Listing first 45 . 100% . 45 ຮເ

summaries

Database PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 29                 | 28     | 27                 | 26                 | 25                 | 24                 | 23                 | 22                | 21                 | 20                 | 19     | 18     | 17                 | 16                 | 15                 | 14                 | 13           | 12                 | 11                 | 10                 | 9                  | 80     | 7                  | 6      | u      | 4                  | ω                  | N                  | 44                 | No.         | Result |
|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|-------------|--------|
| 450.5              | 459    | 460                | 460                | 460.5              | 465                | 467.5              | 470               | 475                | 479                | 481    | 483.5  | 486.5              | 486.5              | 512                | 708.5              | 715.5        | 734.5              | 736.5              | 737.5              | 755                | 767.5  | 784                | 788    | 821.5  | 822.5              | 828.5              | 832                | 3244               | Score       |        |
| 11.9               | 12.2   |                    | 12.2               | •                  | ٠                  | •                  | 12.4              | 12.6               | 12.7               | 12.7   | 12.8   |                    | •                  |                    |                    |              | 19.5               |                    | 19.5               | 20.0               | 20.3   | 20.8               | 20.9   | 21.8   | 21.8               | 21.9               | 22.0               | 85.9               | Match       | Query  |
| 747                | 708    | 760                | 760                | 851                | 828                | 867                | 760               | 863                | 851                | 858    | 854    | 885                | 820                | 863                | 809                | 720          | 729                | 729                | 729                | 753                | 819    | 725                | 725    | 815    | 813                | 826                | 802                | 708                | Length      |        |
| N                  | N      | N                  | N                  | N                  | N                  | 2                  | N                 | N                  | N                  | N      | N      | N                  | N                  | N                  | N                  | N            | N                  | N                  | N                  | N                  | N      | N                  | Ν      | N      | N                  | N                  | N                  | N                  | BB          |        |
| G97408             | A83043 | E85589             | C90739             | AE2129             | S74450             | AC2140             | E64817            | AI2077             | D87252             | AD2421 | AE2082 | AB1944             | AE2130             | AF2074             | S32899             | A36942       | D85673             | H90813             | C64854             | AE0187             | S15169 | H81030             | D81976 | H83345 | A40601             | S41569             | A83125             | B81038             | ID          |        |
| fegA protein U6140 | Ð      | hypothetical prote | hypothetical prote | ferrichrome-iron r | ferrichrome-iron r | ferrichrome-iron r | probable membrane | ferrichrome iron r | TonB-dependent rec | ä      |        | ferrichrome iron r | ferrichrome-iron r | ferrichrome-iron r | ferric-pseudobacti | $\mathbf{r}$ | outer membrane rec | outer membrane rec | ferric-coprogen re | probable iron-side |        | TonB-dependent rec |        |        | ferripyoverdine re | ferric pseudobacti | probable TonB-depe | TonB-dependent rec | Description |        |

| 45                 | 44                 | 43                 | 42                 | 41                 | 40                 | 9                  | 38                 | 37                 | 36                 | S                  | 34                 | 33                 | 32                 | 31                 | 30                 |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 391                | 396.5              | 396.5              | 402                | 407.5              | 411                | 415.5              | 416.5              | 420.5              | 421.5              | 424                | 432.5              | 441.5              | 441.5              | 449.5              | 450                |
| 10.4               | 10.5               | 10.5               | 10.6               | 10.8               | 10.9               | 11.0               | 11.0               | 11.1               | 11.2               | 11.2               | 11.5               | 11.7               | 11.7               | 11.9               | 11.9               |
| 713                | 802                | 710                | 863                | 635                | 714                | 857                | 853                | 853                | 696                | 858                | 732                | 753                | 708                | 872                | 819                |
| N                  | ν                  | N                  | Ν                  | N                  | N                  | N                  | N                  | N                  | N                  | N                  | N                  | N                  | N                  | N                  | N                  |
| E91118             | C83588             | S22673             | S74447             | C81861             | C95382             | AC2132             | S74457             | AC2079             | AC0547             | AE2085             | A83481             | D83081             | AH2626             | AC2134             | AI3197             |
| probable ferrichro | probable hydroxama | ferrioxamine recep | ferrichrome-iron r | hypothetical prote | probable ferrichro | ferrichrome-iron r | ferrichrome-iron r | ferrichrome-iron r | ferrioxamine B rec | ferrichrome-iron r | probable TonB-depe | probable outer mem | ferrichrome iron r | ferrichrome-iron r | TonB-dependent rec |

## ALIGNMENTS

TonB-dependent receptor NMB1829 [imported] - Neisseria meningitidis (strain MC58 serogro C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Bate: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001
C;Accession: B81038
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; pMID:10710307
A;Accession: B81038 A;Molecule type: DNA A;Residues: 1-708 <TET> A;Cross-references: GB:AE002532; GB:AE002098; NID:g7227078; PIDN:AAF42164.1; PID:g722708 A;Experimental source: serogroup B, strain MC58 A; Status: preliminary Genetics: NMB1829

S 덩 á 덩 Ś 片 S 밁 á 밁 ş Query Match Best Local S Matches 627 361 301 301 241 241 181 181 121 121 61 61 Local Similarity les 627; Conserv  $\vdash$ IKOKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIP DLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTFAGRPGCNTADDKACAVGLGTE 360 DWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFA 300 EYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA 180 TVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGY 120 MGQFMSVFRINMTAATVLAALSSSVFAAQTEGLETVHIKGQRSYNAIATEKNGDYSSFAA 60 MGQFMSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAV 60 FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRRETFYAAA FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAA 240 EYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA TVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGY 120 DLKHYFGNGGYGKVGMRYSDRKADSNYTFAGSKLN-----NTG--QADVAGLGTD DWDINPDTVLGAGYLYQQRRLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMHSHDVFA 85.9%; Score 3244; DB 2; ilarity 86.8%; Pred. No. 6.1e-219; Conservative 33; Mismatches 48; Length 708; Indels 14; Gaps 420 300 240 180 ω,

us-09-889-267-2.rpr

| Qy         313 KVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG-CNTADDKACAVGLGTEI 361           Db         396 KLA ADKLWARINMLGLYNDCYYSTTGCASWTQNPGDYSYTDDHD       | Db 724 WR'GGDLATQSKTEDSSTGFQQGGYTVVNAMLGYKVNERIDTRLNFNNLFDKYYYSGIDF 783 Qy 702 ANTFNIPGSERTWTANLRYS 721 Db 784 GN-LNY-GEPRNLMFTVKYS 801 `                                                                                                                          | RESULT 3 841569 ferric pseudobactin M114 receptor protein - Pseudomonas sp. C.Species: Peeudomonas sp. C.Species: Pseudomonas sp. R.Mocris, J.; Donnelly, D.F.; 1994 A.Fitle: Nucleotide sequence analysis and potential environmental distribution of a ferr. A.Freference number: \$41569 MUID:94104606; PMID:8277948 A.Freference number: \$41569 MUID:94104606; PMID:8277948 A.Freference number: \$41569 MUID:94104606; PMID:8277948 A.Fresidues: DNA A.Fresidues: DNA A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresidues: L-826 AND A.Fresid | Query Match  21.9%; Score 828.5; DB 2; Length 826;  Best Local Similarity 29.9%; Pred. No. 8.4e-50;  Matches 227; Conservative 129; Mismatches 303; Indels 101; Gaps 26;  Qy 16 TVLAALSSSVFAAQTADLETVHIKGGRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIPQ 75  115 TVLGAALSSSVFAAQTADLETVHIKGGRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIPQ 75  Db 115 TVLGAALSSSWFAAQTADLETVHIKGGRSYNAIVTEKNGDYSFAVTVGTKIPASLREIPQ 76  Qy 76 SVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYRAGGVSVE-EYNIDGLP 131 |
|----------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Db 349 IKQKAFAVDASYSRPFALGNTANEFVIGADYNRLRSTNEGGRSTLSKSVALDGFRALP 406  Qy 421 QVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSIIGGGRLGHYKIESGEGK 480  :: | RESULT 2 A83125 A83125 Probable TonB-dependent receptor PA4168 [imported] - Pseudomonas aeruginosa (strain PAO1 C; Species: Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 | Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, i. Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathe A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Reference number: AR2950; MID:209950370; PIDN:AAG07555.1; GSPDB:GN001 A;Reference strain PA01 C;Genetics C;Genetics C;Genetics C;Genetics C;Genetics C;Genetics C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal home C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal home Cuery Match Best Local Similarity 30.0%; Pred. No. 4.56-50; Matches 222; Conservative 137; Mismatches 309; Indels 72; Gaps 21;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Qy 19 PALSSSVFAAQTADLETVHIKG-QRSYNAIVTEKNGDYSSFAVTVGTKIPASIREIPQSV 77      :     :                                                                                                                                                                                                                                                                                                                                                                                  |

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C;Keywords: membrane protein
F;184-317/Domain: tonB-dependent receptor
F;538-813/Domain: tonB-dependent receptor
 A;Molecule type: DNA
A;Residues: 1-715,'Y', 717-744,'YN',745-747,'S',749-813 <LAM>
A;Cross-references: EMBL:U07359; NID:g1633044; PIDN:AAB60199.1;
R;MCMorran_B.J.; Merriman, M.E.; Rombel, I.T.; Lamont, I.L.
 C;Species: Pseudomonas aeruginosa
C;Date: 03.May-1994 #text_change
C;Date: 03.May-1994 #sequence_revision 03.May-1994 #text_change
C;Accession: A40601; S54000; PC4227
R;Poole, K.; Neshat, S.; Krebes, K.; Heinrichs, D.E.
J. Bacteriol. 175, 4597-4604, 1993
A;Title: Cloning and nucleotide sequence analysis of the ferripy
A;Reference number: A40601; MUID:93328663; PMID:8335619
 A;Gene: fpvA
C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal
 A;Title: Characterisation of the pvdE gene which is required A;Reference number: JC5090; MUID:97075909; PMID:8918232 A;Accession: PC4227
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 A; Cross-references:
C; Genetics:
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A; Residues: 1-49 < MCM>
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 A; Reference number: A; Accession: S54000
 submitted to the EMBL Data A, Reference number: $53998
 A; Residues: 1-813 < POO>
 ferripyoverdine receptor - Pseudomonas aeruginosa
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 A; Cross-references: GB:L10210; NID:g294360;
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 A;Status: preliminary
 A; Accession: A40601
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 1994
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 for pyoverdine
 PID: g466459
 29-Sep-1999
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Query Match
Best Local Similarity
Matches 215; Conserv
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 ASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNI 127
 VGGANTFNI PGSERTWTANLRYSF
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 EISGAVTPKWOIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQ----VTPELTI
 FEVGYKGSYMDDRLNARVSFYRMKDKNAAAP-----LNPNNKKTRYAALG-KRVMEGVET
 GLNPTIRESG--RFIPYVGAVYDLNDTYSVYASYTDIFMPQDSWYRDSSNKLLEPDEGQN
 GEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTN--LDADGKLLKPRQGNQ
 ----INWDGDIGKPDWGTPSQYIDDKTROLGSYMTARFNVTDDLNLFLGGRVVDYRV-T
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 21.8%; Score 822.5; DB 2; 28.9%; Pred. No. 2.1e-49; tive 145; Mismatches 317;
 Indels
 Length
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 Gaps
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrene adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kal.; LOTY, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83345
A;Status: preliminary ferripyoverdine receptor PA2398 [imported] - Pseudomonas aeruginosa (strain c;Species: Pseudomonas aeruginosa (strain c;Species: Pseudomonas aeruginosa (strain c;Species: Pseudomonas aeruginosa (strain c;Spate: 15-Sep-2000 #sequence revision 15-Sep-2000 #text\_change 31-Dec-2000 C;Accession: H83345 A;Molecule type: DNA ; Warrener, K.R.; Kas, an ₽ 'P : : opportunistic Hickey, Larbig,

RESULT 5 H83345

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A;Residues: 1-725 cPAR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83866.1; PID:g737931
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NWA0575
A;Reference number: A81775; MUID:2022556; PMID:10761919
A;Accession: D81976
A;Status: preliminary
A;Resichiner. Presidential Agenta and Agenta menigitidis 22491.
 Query Match
 176
 234
 175
 235
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 GB:AE004091; NID:g9948438; PIDN:AAG05786.1; GSPDB:GN001
 amino-terminal
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 DGLPAQMQSI----NGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQG 183
 HAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWD 243
 244 INPDTVLGAGYLYQQRHL--APYNG-LPA-DANNKLPSLPQHVFVGADWNKFKMNSHDVF 299
 RSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIES 476
 :: ; | | | :: ; | | :: ; | | :: ; | | :: ; | | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ; | :: ;
 GEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTN--LDADGKLLKPRQGNQ 534
 535 FEVGYKGSYMDDRLNARVSFYRMKDKNAAAP----LNPNNKKTRYAALG-KRVMEGVET 588
 EISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQ---VTPELTI 645
 GGGV-----NAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNR 693
 108 FQGNAITISVAEAADSSV-----DLGATMITSNQL--GTITEDSGSYTPGTIATATRLV 159
 ASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNI 127
 ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGT 359
 Gaps
 FRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIP 67
 EIKOKALAFDASYSRPFRLGNTANEFVIG--ADYNRFRSTNEOGRITLYARG-GLALNEF
 A;Residues: 1-815 <>...
A;Cross references: GB:AE004666; GB:AE004091; Nlu:gy>+v---,
A;Eross references: GB:AE004666; GB:AE004091; Nlu:gy>+v---,
A;Ecnetics: Strain PAO1
C;Genetics: A;Gene: fpvA; PA2398
C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor
C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor
 Query Match 21.8%; Score 821.5; DB 2; Length Best Local Similarity 29.0%; Pred. No. 2.5e-49; Matches 217; Conservative 145; Mismatches 312; Indels
 694 HYYARVGGANTFNIPGSERTWTANLRYSF 722
 | | : | : | | : | | 188 TYTUIGFYTSASY-GDPRNLMFSTRWDF 815
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 340
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 68
 160
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 23;
 ETFYAAADWDINPDTVLGAGYLYQQRHL---APYNGLPADANNKLPSLPQHVFVGADWNK 290
 SRHRALNLFAGIEHRFN------QDWKLKAEYDYTKSR--FRQPYGVAGVLSIDH 341
 351 KACAVGL---GTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYA 407
 ANLWITYQVIPEL----TIGGGV------NAMSGIISSAGMHAGGYAIFD 670
 FAVIVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQ-LARKTPGLRVLSNDD--GRSS 114
 AELYGILEYDIAPQTRVHAGMDYQQAKETADAPLSYAVYDSQGYATAFGPKDNPATNWAN 294
 408 RGGLALNEFRSIPQVDLIANARKGVRGYSHTVA-----TENLDEFGI-----YGKST 454
 AMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIP-----GSERTWTANLRYSF 722
 724
 S MSVFRINMTAATVL-----AALSSSVFAAQTADLETVHIKGORSYNAIVTEKNGDYSS
 VYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR
 KRPTKAFQGHAAAGFGTHKQYKABADVSGSLNSDGSVRGRVMAQ-TVGASPRPAEKNNRH
 291 FKWINSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADD
 342 NTAATDLIPGYWHADPRTHSASVSLIGKYRLFGREHDLIAGINGYKYAS-NKYGE----
 FHPADGLSLIGGGRLGHYKIESGEGKT -- LHKASKTKFTGYAGAVYDLNDNNSLYLSLSQ
 FRAADNLSLILGGRYSRYRTGSYDSRTQGMTYVSANRFTPYTGIVFDLTGNLSLYGSYSS
 LYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKN--AAAPLNPNN
 KKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHS
 FKL FTAYHFAPEAPSGWTIGAGVRWQSETHTDPATLRI PNPAAKARAADNSRQKAYAVAD
Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor
 20.9%; Score 788; DB 2; Length 725; illarity 29.9%; Pred. No. 4.7e-47; Conservative 117; Mismatches 316; Indels 112;
 Best Local Similarity
Matches 232; Conserva
 671
 677
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RESULT 7

D81976
probable ferric siderophore receptor protein NMA0575 [imported] - Neisseria meningitidia
C;Space: Serial meningitidis
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001
C;Accession: D81976
C;Accession: D81976
F; Accession: D81976
F; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

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H81030 Tonb-dependent receptor NMB1882 [imported] - Neisseria meningitidis (strain MC58 serogrow C;Species: Neisseria meningitidis

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678

MARYRFNPRAELSLNVDNLFNKHYRTQ-----PDRHSYGALRTVNAAFTYRF

724

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A;Gene: NMb155,
C;Superfamily:
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: H81030 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755; PMID:10710307 A;Accession: H81030
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 A; Molecule type: DNA
A; Residues: 1-725 < TET>
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 A; Experimental source: serogroup
 A; Cross-references: GB: AE002538;
 A; Status: preliminary
 Query Match
Best Local S
Matches 228
 ;Gene: NMB1882
 514
 236
 176
 672
 618
 503
 443
 456
 396
 409
 343
 352
 296
 292
 235
 175
 116
 115
 56
 58
 Local Similarity
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 HPADGLSLIGGGRLGHYKIESGEGKT---LHKASKTKFTGYAGAVYDLNDNNSLYLSLSQL
MAAYRETPKLKLQINADNIFNRHYYARVGGANTFNIP-----GSERTWTANLRYSF
 NLWTTYQVTPEL---TIGGGV---
 KTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSA 631
 YTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKN--AAAPLNPNNK
 RAADNLSLILGGRYTRYRTGSYDSRTQGMTYVSANRFTPYTGIVFDLTGNLSLYGSYSSL
 ACAVGL---GTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYAR
 RHRALNLFAGIEHRFN-
 ELYGILEYDIAPQTRVHAGMDYQQAKETADAPLSYAVYDSQGYATAFGPKDNPATNWANS
 TEYAAADWDINPDTVLGAGYLYQQRHL---APYNGLPADANNKLPSLPQHVEVGADWNKF
 LFARGSRI ANYQINGI PVADALADTGNANTAAYERVEVVRGVAGLLDGTGEPSATVNLVR
 VYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR 174
 SGTHTPLGLPWTLREIPQSVSVITSQQWRDQNIKTLDRALLQATGTSRQIYGSDRAGYNY
 MSVFRINMTAATVL-----AALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSS
 KLFTAYHFAPEAPSGWT1GAGVRWQSETHTDPATLR1PNPAAKARAADNSRQKAYAVAD1
 NTYYRAANQAKTHGWEIEVGGRITPEWQIQAGYSQSKTRDQDGSRLNPDSV----
 FVPQSQKDEHGSYLKPVTGNNLEAGIKGEWLEGRLNASAAVYRARKNNLATAAGRDPSG-
 GGLALNEFRSIPQVDLIANARKGVRGYSHTVA----TENLDEFGI-----YGKSTF
 TAATDLIPGYWHADPRTHSASVSLIGKYRLFGREHDLIAGINGYKYAS-NKYGE-----
 KMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDK 351
 KRLTRKPLFEVRAEAGNRKHFGLDADVSGSLNTEGTLRGRLVSTFGRGDSWRRRERSRDA
 KRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHE
 FAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQ-LARKTPGLRVLSNDD--GRSS 114
 MTRFKYSLLFAALLPVYAQADVSVSDDPKPQESTELPTITVTADRT-----ASSNDGYTV 55
 228;
 ferric-pseudobactin receptor; tonB-dependent receptor
 Conservative
 - ŔŚI - - - - I PŃAI PNAYEF ŚRTGAY POPAS FAOTI POYGTRROIGGYLATR F
 20.8%;
29.4%;
 118;
 GB:AE002098; NID:g7227136; B, strain MC58
 Score 784; DB 2;
Pred. No. 8.9e-47;
.8; Mismatches 320
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 -NAMSGITSSAGMHAGGYATFDA 671
 Length
 Indels
 PIDN:AAF42216.1;
 110;
 Gaps
 amino-terminal hom
 408
 342
 291
 235
 234
 115
 57
 571
 502
 442
 455
 395
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 617
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 513
 21;
 PID:g72271
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A;ACCESSIONA
A;Molecule type: DNA
A;Residues: 1-819 <BIT>
~~~~~references: EMBL:X56605; NID:g45722; PIDN:CAA39942.1;
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A;Accession: S15169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Bitter, W.; Marugg, J.D.; de Weger, L.A.; Mol. Microbiol. 5, 647-655, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: S15169
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993
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Best Local Similarity
Matches 214; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Keywords: membrane protein
;1-47/Domain: signal sequence #status predicted <SIG>
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660
                                     895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---PNNKKTRYAALGKRVMEGVET----EISGAVTPKWQIHAGYSYLHSQIKTASNSRD
                                                                           ASYTDIFKPQNNVDITGKPLDPEVGKNYELGWKGEFLEGRLNANIALYMVKRDNLAESTN
                                                                                                                                                    RFNLTDDLHLILGARASNYRFDYALWRIGNEPAPYKMVERGVVTPYAGIVYDLTNEQSVY
                                                                                                                                                                                     TFHPADGLSLIGGGRLGHYKIE-----SGEGKTLHKASKTKFTGYAGAVYDLNDNNSLY
                                                                                                                                                                                                                                                                                                                                         GCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPA----DANNKLPSLPQHVFVGADWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDGVTTYQDNQTRNMPSTLMDVGLYDRIEIVRGATGLMTGAGDPSAVVNVIRKRPTREFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDGLPA----QMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSIRETPQTITVVTRQRMDDQHLGSMNEVLTQTPGI-TMSQDGGERFNIYSRGSAINIYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDG-RSSVYARGYEYSEYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YQIDGNTVTVTASA-----AAKDGQIELSATNVNSAGLGETTEGTGSYTTRVTSTATKMN
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EVVPDSG----GLIASRAVDGAETKGVDVELSGEVLPGWNVFTGYS--HTRTEDADGKR-
                                                                                                            LSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLN
                                                                                                                                                                                                                                                                TLYARGGLALNEFRSIPOVDL-----IANARKG----VRGYSHTVATENLDEFGIYGKS
                                                                                                                                                                                                                                                                                                      YLELDGSTEISAGIVT-AKOHOKGVDATLOGPFQLLGQTHELIVGYNYLEYENKH-----
                                                                                                                                                                                                                                                                                                                                                                                                                    KFKMNSHDVFADLKHYFG-----NGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRP
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27.8%;
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Pred. No. 1.5e-45;
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NyAlternate names: outer membrane protein fhuE
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: CG4854; S09262; A26875; PC4409
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Mosidues: 1-729 SBLAT
A,Rosidues: 1-729 SBLAT
A,Experimental source: strain K-12, substrain MG1655
A,Experimental source: strain K-12, substrain MG1655
Mol. Microbiol. 4, 427-437, 1990
A,Title: Sequence of the flub outer-membrane receptor gene of Escherichia coli K12 and p)
A,Reference number: S09262; MUID:90286919; PMID:2162465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title: Ferric-coprogen receptor FhuE of Escherichia coli: processing and sequence communications number: A26875; MUID:87194585; PMID:3032906
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A;Residues: 1-69 <SA2>
R;Kobayashi, Y.; Sasanuma, A.; Nishimura, A.; Kuratomi, K.
Rese. Commun. Biochem. Cell Mol. Biol. 1, 157-170, 1997
A;Title: A novel 14-kilodalton protein in Pl,P4-bis(5'-adenosyl)tetraphosphate (Ap4A)-bin
A;Reference number: JC5685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A bescription: required for uptake of iron(III) via coprogen, ferrioxamine B and rhodoto (S. Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolog (C. Superfamily: ferrichrome-iron membrane protein; receptor B: 136/Domain: signal sequence #status predicted <SIG> F:1-36/Domain: signal sequence #status predicted <SIG> F:37-729/Product: outer membrane protein fhuE #status predicted <MAT> F:97-230/Domain: tonB-dependent receptor amino-terminal homology <TNN> F:462-729/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>
510 FVPYSGLTYDINRDLSVYTSYTEIFNPENRRDRNNTLLAPVSGQNYEAGLKGVAFDNSLD 569
                                                                                                                                                                                                                                                                                                     A.Residues: 1-362, C, 364-729 <SAU>
A.Cross-references: EMBL:X17615, NID:941448; PIDN:CAA35616.1; PID:941449
A.Experimental source: strain K.12
                                                                                         SYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQV---TPELTIGGGVNAMS----GITS
                                                                                                                                                                                                SAGMH---AGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTW
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A, Residues: 1-47 < KOB>
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                                                                                                                                                                                                                                                                                                             probable iron-siderophore receptor YPO1537 [imported] - Yersinia pestis (strain CO92)
C; Species: Yersinia pestis
C; Species: Yersinia pestis
C; Species: Yersinia pestis
C; Species: Yersinia pestis
C; Species: Yersinia pestis
C; Species: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C; Accession: AE0187
R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Citilingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A; Reference number: AB0001; MUID:21470413; PMID:11586360
A; Accession: AE0187
A; Stetus: preliminary
A; Molecule type: DNA
A; Residues: 1-753 acure
A; Cross-references: GB:AL590842; PIDN:CAC90360.1; PID:g15979580; GSPDB:GN00175
C; Genetics:
A; Gene: YPOL537
C; Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal home
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                                                             225 RPAEKN----NRHE----TFYAAADWDINPDTVLGAGYLYQQRHL---APYNGLPA-DANN 273
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                           DGIFLLMPKHSANLWTTYQVTPE---LTIGGGVNAMSGITSSAGMH-----AGGYATFDA 671
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                                                                                                                                                                  RINMT----AATVLAALSSSVFAAQTADLETVHIKGQRSYN-
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27.3%;

C;Genetics:
A;Gene: ECs1480
C;Superfamily: f

ferric-pseudobactin receptor; tonB-dependent receptor

amino-terminal

homo

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A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H90813
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-729 <hAY>
A;Cross-references: GB:BA000007; PIDN:BAB34903.1; PID:g13360944; GS
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                        R;Hayashi, T.; Makino, I
gasawara, N.; Yasunaga,
DNA Res. 8, 11-22, 2001
                                                                                                                                                                                          outer membrane receptor for ferric iron uptake BCs1480 [imported] - Escherichia C;Species: Bscherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: H90813
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                                                                                                                                                        Makino, K.; Ohnishi,
Yasunaga, T.; Kuhara,
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8; Mismatches 308;
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                                                                                                                                                        Kurokawa, K.; Ishii, K.; Shiba, T.; Hattori, M.; S
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outer membrane receptor for ferric iron uptake [imported] c;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_c
C;Accession: D85673
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C A;Title: Genome sequence A;Reference number: A8548 A;Accession: D85673 nence of a enterohemorrhagic Escherichia MUID:21074935; PMID:11206551 Mau, B.; Glas A.; Dimalanta, #text\_change Glasner, lanta, E.; coli 0157:H7 J.D.; Rose, Potamousis, 14-Sep-2001 D.J.; (strain Apodaca Mayhew

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M.J.; Br K.; Lim,

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J. Bacteriol. 176, 307-319, 1994

A; Title: FptA, the Fe(III)-pyochelin receptor of Pseudomonas aeruginosa: a phenolate shreference number: A36942; MUID: 94117363; PMID: 8288523

A; Status: preliminary
A; Status: preliminary
A; Multiple: DAMA
A; Status: preliminary
A; Multiple: DAMA
A; Status: preliminary
A; Residues: 1-720 < AANX
A; Cross-references: GB: U03161; NID: 9454352; PIDN: AAC43213.1; PID: 9454353
B; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, X.; Pham, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Listure 406, 959-964, 2000
                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-720 <STO>
                                                                                                                                                                                                                                                                      A;Status: preliminary
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                                                        PIDN: AAG55848.1; GSPDB:GN00145; UWGP:Z17
                                                                                                                             amino-terminal
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                                                                                                                                                                                                                                                                                                                           68 GTKMQMTQRDIPQSVTIVSQQRMEDQQLQTLGEVMENTLGISKSQADSDRALYYSRGFQI 127
                                                                                                                                                                                                                                                                                                                                                                                                KAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGA---SPRPAEKNNRHET 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---AGRPGCNTADDKACAVGLGTE----IKQKALAFDASYSRPFR--LGNTANEF--V 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTKIPASLREIPOSVSIITNOOVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYAA-ADWDINPDTVLGAGYLYQQRHL--APYNGLPA-DANNKLPSLPQHVFVGADWNKF 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIFILIMPKHSANLWTTYQ--VTPELTIGGGVNAMSGITSSA-----GMHAGGYATFDA 671
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                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                        11 QYQAITKPSLLAGCIALALLPSAAXAAPATEETVIVEGSAT---APDDGENDYSVTSTSA 67
                                                                                                                                                                                                                                   QFMSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFKGDVSAEYGSWNKERYVADLQSPLTEDGKIRARI----VGGYQNNDSWLDRYNSEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKEINKVFMTLKQRFADTWQATLNATHSEVEFDSKMMYVDAYVNKADGMLVGPYSNYGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 IGSFYN-FNG------WSPQSLAQDDTTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 TYASYTSIFQPQNDRDSSGKYLAPITGNNYELGLKSDWMNSRLTTTLAIFRIEQDNVAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEYNIDGLPAQMQS---INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 KWNSHDVFADLKHYPGNGGYGKVGMRYSDRDADSNY----AFAGSKLGMKTP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDYVGGTGWNSGKRKVDALDLFADGSYELFGRQHNLMFGGSYSKQNNRYFSSWANIFPDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F-GIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAA--
                                                                                                                             receptor
                                                                                                                                                                                               Indels 103;
                                                                                                                                                              DB 2; Length 729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      672 MAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: ferric-pseudobactin receptor; tonB-dependent
 A;Status: preliminary
A;Molecule type: DNA
A;Resides: 1-729 <STO>
A;Cosides: 1-729 <STO>
A;Cosides: 1-729 <STO>
A;Cosides-references: GB:AE005174; NID:g12514649; PIDN:AAC
A;Experimental source: strain O157:H7, substrain EDL933
C;Generics:
C;Generics:
C;Superfamily: ferric-pseudobactin receptor; tonb-depend
                                                                                                                                                            Query Match 19.5%; Score 734.5; DB 2; Best Local Similarity 27.1%; Pred. No. 2.6e-43; Matches 209; Conservative 146; Mismatches 313;
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C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal homo F;98-227/Domain: tonB-dependent receptor amino-terminal homology <TNN> F;446-720/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                            GB:AE004091; NID:g9950434; PIDN:AAG07609.1; GSPDB:GN001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|:|| || || |:: |:|||| :| |
DRYRAEVDVGGPLSASGNVRGRAVA---AYEDRDYFYDVADQGTR--LLYGVTEFDLSPD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVLGAGYLYQQ-RHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYF 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKAL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 AFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNBFRSIPQ--VDL 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLDANLNGPVRLFGLTHELLGGVTYAQGETRQDTAR------FLNLPNTPVNV 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 IANARKGVR----GYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGK 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPKWQIHAGYSYLHSQ-IKTASNSRDDGIFLLMPKHSANLWTTYQV---TPELTIGGGVN 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 IPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNIDGLPA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLRE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLLTVGAQYQHIDSITNMAGVPMAKDGSNLGLSRDTYLDVDWDRFKWDTYRAFGSLEQQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGSYMDDRLNARVSFYRMKDKNAAA-----PLNPNNKKTRYAALGKRVMEGVETEISGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRP----AEKNNRHETFYAAADWDINPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.9%; Score 715.5; DB 2; Best Local Similarity 27.2%; Pred. No. 5.5e-42; Matches 200; Conservative 137; Mismatches 323;
                                                                                                                                                                                                     A;Cross-references: GB:AE004839; Gi
A;Experimental source: strain PAO1
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셤 ò 8

A36942
Fe(III)-pyochelin receptor fptA precursor - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 31-Dec-2000
C;Accession: A36942, G83117
R;Ankenbauer, R.G.; Quan, H.N.

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RESULT 14
$33.899
$crric-pseudobactin receptor pupB precursor - Pseudomonas putida
C;Species: Pseudomonas putida
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
C;Accession: $32.899
R;Koster, M.; van de Vossenberg .T. Lagrage T. Maideler.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: pupB
A;Start codon: GTG
A;Start codon: GTG
C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor an
C;Keywords: membrane protein
C;Keywords: nembrane protein
F;1-45/Domain: signal sequence #status predicted <SIG>
F;46-809/Product: ferric-pseudobactin receptor #status predicted <MAT>
F;189-119/Domain: tonB-dependent receptor amino-terminal homology <TNN:
F;543-809/Domain: tonB-dependent receptor carboxyl-terminal homology <
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A;Cross-references: GB:
C;Genetics:
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Best Local Sim
Matches 197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koster, M.; van de Vossenberg, J.;
ol. Microbiol. 8, 591-601, 1993
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                                 GKSTFHPADGLSLIGGGRLGHYKIES----
                                                                       TPSWGGWRYDYAGSPAGAIDNLFNWDGKSAKPAFVESGKSSI-
                                                                                                                                                                                                                                                                                           SQLMYGITEFDLSEDTLLTVGFSYLRSDIDSPLRSGLPTRFSTGERTNLKRSLNAAPDWS
                                                                                                                                                                                                                                                                                                                           HETFYAAADWDINPDTVLGAGYLYQQRHL-APY-NGLPAD-ANNKLPSLPQHVFVGADWN
                                                                                                                                                                                                                                                                                                                                                                                                VRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNR
                                                                                                                                                                                                                                                                                                                                                                                                                                        DSYWSRGFAIQNYEVDGVPTSTR-LDNYSQSMAMFDRVEIVRGATGLISGMGNPSATINL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDIDQGLAILLAGTGLEASRGANASYSLQASASTGALELSAVSISGKAP--GSTTEGTGL
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LTSRFSVTDDLSLILGSRLINWKRDTSDRPYGGEETEVNREENGVFIPYAGVGYDLDDTW
                                                                                                                                                                               TADDKACAVGLGTEIKQKALAF-----
                                                                                                                                                                                                                     ---YNDHEQTSFFTSIEQQLGNGWSGKIELTHAENKFDELFNFA---MGELNPD
                                                                                                                                                                                                                                                       KFKMNSHD---VFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCN
                                                                                                                                                                                                                                                                                                                                                              IRKRPTAEAQASITGEAGNWDRYGTGFDVSGPLTETGNIRGRFVADYKTEKAWIDRYNQQ
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                                                                                                       NEQGRTTLYARGGLALNEFRSIPQVD-----LIANARKGVRGYSHTVATENLDEFGIY
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                                                                                                                                             -GSGLSQLPVRFSGTPRQDNLDLYATGPFSLFGREHELITGMTLSQYREN
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25.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 708.5; DB Pred. No. 2e-41;
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                                                                                                                                                                               DASYSRPFRLGNTANEFVIGADYNRFRST
                                 GEGKTLHKASKTKFTGYAGAVYDLNDNN
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Wata Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yas DNA Res. 8, 205-213, 2001
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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AF2074
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A;Molecule type: DNA
A;Residues: 1-863 <KUR>
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C; Superfamily:
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Best Local Similarity
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 434
                                    516 GKFNTGSISHQILIGFDFNHNIDT------FARVVQRNVPNLD-IFNPNYNIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLYLSLSQLYTPQTN--LDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA
                                                                                                                                                SNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSR-----
                                                                                                                                                                                                                                                                                                                                                                 GPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGF--GTHKQYKAEADVSGSLNSDGSVR 212
                                                                                                                                                                                                                                                                                                                                                                                                         DGADYNGSPAQDFIIRGFEQGGSFRNGYRDVNSYGLTGV-----GTI-----ERVEVLK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                            SNDDGRSS----VYARGYE-----YSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMR 154
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                                                                                                                                                                                                                       ANNKLP-----SLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDR-DAD
                                                                                                                                                                                                                                                                                                GRVMAQTVGASPRPAEKNNRHETFYAAADWDI--NPDTVLGAGYLYQQRHLAPYNGLPAD
                                                                                                                                                                                                                                                                                                                                  GPASVLFGAVEPGGIINVVTKQPLS--EPYYQLGFEVGNRAFYQPSIDFSGPLNADKTLL
GYSH---TVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGE--
                                                                         - PFRIGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVR
                                                                                                                                                                                                                                                           YRFNASYQSSDGFQDFVNTNLTTIAPTIAWKLGDRTDLTLYYEYINFKGTFEQYTSILSD
                                                                                                                                                                                  -NTFLPRSFYQAYPNNAYVDNTTQKL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ferrichrome-iron receptor 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Wolk, C.P.; Kuritz, T.; Sugimoto, M.; Takazawa, 1
                                                                                                             -NAEEYTLATGVVNDQSLRQFAQDREFTQDNYFGQIDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 512; DB 2;
Pred. No. 1.3e-27;
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, M.; Yasuda, M.;
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
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C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:BA00019; PIDN:BAB73058.1; PID:g17130447; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics:
                                                                                                                                                                                                                                                                                                                                    GAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFL----LMPKHSANLWTTYQVTPELTIG 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            734 -----QSGDLKGLGFGLGLYYVGDRYADVENTSLLSSYFRTDSAIYYKRDNWRLALNFRN 788
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                        358 G-TEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEF
                                                   516 NPNYDVELPATPDESTFSY----TTREDILGIYVQDQITFADNLKLLVGGRFDAFQRKE
                                                                                                                                                                                                                                            OPEVGYKGSYMDDRLNARVSFYRMKDKNAAA--PLNPNNKKTRYAALGKRVMEGVETEIS
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                                                                                                                     RSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHY-KIE
                                                                                                                                                                                                               SGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQT - - NLDADGKLLKPRQGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                647 GGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             690 IFNRHYYARVGGANTFNIPGSERTWTANLRYSF
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C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-22001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AE2130
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2130
A;Accession: AE2130
A;Accession: AE2130
A;Accession: AE2130
A;Gratus: prellminary
A;Molecule type: DNA
A;Residues: 1-820 «KUR»
A;Residues: 1-820 «KUR»
A;Residues: 1-820 «KUR»
A;Cross-references: GB:BA000019; PIDN:BAB74295.1; PID:g17131689; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all-2596
C;Genetics:
A;Gene: all-2596
C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
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                                                                                                                                                                 LNARVSFYRMKDKNAAAPLNPNNKKTRYAAL-----GKRVMEGVETEISGAVTPKWOIH 601
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SPDYGPRSSSTERFQTYGIYLQDQITFLDNLKLLIGGRFDWISGENTDNVTGDTTQNPDS 621
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                                                                                                 SAFSPRIGLVYQPSKSVSLYTSYSQSFVPETGVNPDGEIFEPTRGTQYEAGIKADFLEGR
                                                                                                                                                                                                                                                             AGYSYLHSQIKTASNSRDDGIFLL-MPKHSANLWTTYQVTPE----LTIGGG---VNAMS
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12.9%; Score 486.5; DB 2; Length 820;
Best Local Similarity 24.6%; Pred. No. 7.1e-26;
Matches 185; Conservative 112; Mismatches 353; Indels 103;
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Wata Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yas DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2082
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A;Residues: 1-854 <KUR>
A;Residues: 1-854 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73910.1; PID:g17131302; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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C;Species: Nostoc sp.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KILLGGRFDIISQKQEDDNGETINFLQDEAFSPRIGLVYQPTKNISLYGSYSRSFTQVVG
                                                                                                                                                                                                        LAALSSSVFAAQTADLETVH-----IKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AALNINNLFDTEYFETAFDALSV-VPGA 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOINADNIFNRHYYARVGGANTFNIPGS 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGEQRSQGIELDIAGEILPGWKIIGGYAY--SDAKVTQDQEFEGNLLNNTPKHAFSLWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAA--PLNPNNKKTRYAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NERYFISPVLTWLIDKNTNLTLEAEYLSTKN--PNYNGLPA-LGTVLPNPEGEIPLSRNL
  GLRNGFKDFGFTSPRDVANIERVEFLKGPASVLYGSANNPGGVVNTITKKPLPDPSYRVG
                                      GLPAQMQSINGTLPNLFA-FDRVEVMRGP-SGLFDSSGEMGGIVNLVRKRPTKAFQGHAA
                                                                                 RDIPASVQVIPKEIIQDRQVVRLNELANNVSGVQQQSGYGGLSSSGYFIRGF---ESGFE
                                                                                                                        REIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSS--VYARGYEYSEYNID 128
                                                                                                                                                               LAPIASTIPAPEQPEQPTSETPPAQPTAENNEPIELVVTGNQDQYRVEESSTATKIDAPL 216
                                                                                                                                                                                                                                                   183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y----ELQSGN----LQGLGFGLGLYYIGERQGDLSNSFELPSYFRTDAAMFYR-RNNFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YQVTPELTIGGGVNAMSGITSSAGMHAGG-----YATFDAMAAYRFTPKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFL-LMPKHSANLWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLIGGGRLG--HYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDFAIE----PINLFNPVYGTQTIGSSAPSSNFISNT-----DGLGIYLQDQMTLADNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGL 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -EDNRTLVRFAQSLESTRNVYVLNTNVVGDFKTGSIAHKLLFGFDLLRDDTRNRDT
                                                                                                                                                                                                                                                                                                                               ferrichrome-iron receptor 1; tonB-dependent receptor
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguo
S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
                                                                                                                                                                                                                                                 12.8%; Score 483.5; DB 2; 24.1%; Pred. No. 1.2e-25; tive 134; Mismatches 328;
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30-Jun-2002
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C;Species: Nostoc sp. Atrain PCC 7120 is a synonym of A;Note: Nostoc sp. Strain PCC 7120 is a synonym of C;Date: 14-Dec-2001 #sequence revision 14-Dec-2001 C;Accession: AD2421
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                                                                                                                                                                                                                                                                                                                                            RGLELDIAGEILPGWKIIATYAYIDSSVSKDNDLERLNDRLSGV----PRNSASLWTTYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKLLKPROGNOFEVGYKGSYMDDRINARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFFSAPIASIDIFNPVYGAQPGTFDRSFAGEYGGDNL---AVYFQNLIEFTPNLKLLAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFRSIP--QVDL---IANARKGV--RGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGG
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                                                                                                                                                                                    INIKNLEDTEYYE----SQSFYLVPAAPLTVLGTISFEF
                                                                                                                                                                                                                         INADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF
                                                                                                                                                                                                                                                                                                       VTPELTIGGGVNAMSGITSSAGM-----
                                                                                                                                                                                                                                                                                                                                                                                 EGVETEISGAVTPKWQIHAGYSYLHSQIKTAS----NSRDDGIFLLMPKHSANLWTTYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFDWIDSFDRDPVSNTVNNEVSESNFSPRVGIVYQPTNSTSLYASWTNSFNPQFFGRSRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R---LGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQ-TNLDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EHOFSDDWKFROGFNVTSIRGNTRIA-RNTNFSEPFLEDDGOTLPR---TSETSDEEQEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISPKTSMTFEYEYQKYNYTFDRGLL--PGNTFFQIPISRFLGEPGFNNAEFISNVFTYNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INPUTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG-ADWNKFKMNSHDVFADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGFGTHKQYKAEADVSGSLNSDGSVRGRV-MAQTVGASPRPAEKNNRHETFYAA--ADWD
                                                                                                                                                                                                                                                                FQK-----GSLAGLGFGLGLVYVDEREATLPNTIKIPSYVRTDASIFYR-RDNWRAA
                                                                                                                                                                                                                                                                                                                                                                                                                        GESFKPETSEQFEVGIKQEFFDKRLSATLAYFDITKNNVLTPDPVDNNFS---VQIGEQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYGKVGMRYSDRDADSNYAFAGSKL---GMKTPAGRPGCNTADDKACA
                                                                                                                                                                                                                                                                                                       ---HAGGYATFDAMAAYRFTPKLKLQ
                                                                                                                                                                                      854
                                                                                    (strain PCC 7120)
                  Anabaena sp. strain PCC '
#text_change 30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                   638
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                                           PCC 7120
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A;Gene: all4924
C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor
                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-858 - KKIR>
A;Cross-references: GB:BA000019; PIDN:BAB76623.1; PID:g17134062; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                            A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: AD2421
                                                                                                                                                                                                                                                                                                                                                                                                      Nakazaki, N.; Shimpo, S. DNA Res. 8, 205-213, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                          R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada,
                                                                                                                                                                                        A; Experimental source: strain PCC C; Genetics:
17 VLAALSSSVFAAQTADLETVHIKGQ-----RSYNAIVTEKNGDYSSFAVTVGTKIPASL
                                                                       Local Similarity
                                              Conservative 127;
                                                                    12.7%; Score 481; DB 2; 25.2%; Pred. No. 1.8e-25;
                                                   Mismatches
                                                                                             DB 2;
                                                                                          Length 858
                                                 Indels
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                                                                                                                                         amino-terminal
                                              Gaps
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                                                 27;
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REIPQSVSIITNQQVKDRNVDTFDQLARKTPGLR-VLSNDDGRSSVYARGYEYSEYNI--LIVAVTSAKVAMQPP--ETPAIPEQPAAQPDEPIELVVTGEQDQYRVPAASVGTRTDTPL

216

homol

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A. Accession: Also C. 7120 is a synonym of Anabaena sp. strain PCC 7120 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C; Accession: AL2077 R; Accession: AL2077 R; Askamura, Y:; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res B, 205-213, 2001 A; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S A; Reference number: AB1807; WUID:21595285; PMID:11759840 A; Reference number: AB1807; WUID:21595285; PMID:11759840 A; Prefixing Cyanobacterium Anal A; Reference number: DRA Prefixing Cyanobacterium Anal A; Molecule type: DNA A; Residues: 1-863 <KUR>
                                                                                                                                                                                                                                                                                                                         : | | : | | | | 310 DRRSFYGVASKDYQKTKSDIATFA-IDHRIDETLNLRQVVRYSKSLNDYIVTNPGDGGAA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -FAGSKLGMKTPAGRPGCNTADDKACAVGLGTE1--KQKALAFDASYSRPFRLGNTANEF 385
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                         ---GTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGR---SSVY
                                                                                                ARGYEYSEYN -- IDGLPAOMOSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR
                                                                                                                                                                       KRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASP-RPAEKNNRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OFVOGOWWKR-----GIKTRWNPIETVAAVTDLHGKKTFLGLEHSFDVGLELSREEN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 VIGADYNRFRSTNEQ-----GRITLYARGGLALNEFRSIPOVDL---IANARKGVRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHIVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKTTA------LYGFDTVKFGEKVLLNLGLRHDRYESKGVDVATTQANGVFTSVTYTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              530 ROGNOFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       590 ISGAVTPKWQIHAGYSYLHSQ-IKTASNSRDDGIFLL-MPKHSANLWTTYQVTPELTIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GV----NAMSGITSSAG-----MHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       484 KASKTKFTGY-AGAVYDLNDNNSLYLSLSQLYTP-----QTNLDADGK-----LLKP
 INMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSF-AVTV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ferrichrome iron receptor [imported] - Nostoc sp. (strain PCC 7120)
C,Species: Nostoc sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGGANTFN-IPGSERTWTANLRY 720
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D87252
Tomb-dependent receptor [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: D87252
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Restdues: Dreliminary
A;Molecule Lype: DNA
A;Restdues: 1-851 <STO>
A;Cross-references: GB:AE005673; NID:g13421118; PIDN:AAK22016.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0028
C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
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|:|||||: :: | :::: | ::: | ::: | RDIPQSIQVVPRQVIGEGRADSFTIRGFEIFSGNVLN 276
                                                                                                                               244
                                                                                                                                                      331 IEATVGNYDLYRGGIDFSCPLNDSKTLLYRLNLAYQNSGSYIDFVGNRSFFIAPVISAAL 390
                                                                                                                                                                                                                                                                                                      414 NEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADGLSLIGGGRLG 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                       546 AELTPLDIYNPV--YRQPIVGRIDAVYEDNSRLTDTLGIYIQDQIKFAENFQLLLGGRPD 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              691
                                                                                                                                                                                                      245 NPDTVLGAGYLYQQRHLAPYN--GLPADANNKLPS-----LPQHVFVGADWNKFKMNSHD 297
                                                                                                                                                                                                                                                                               298 VFADLKHYFGNGGYGKVGMRYS-DRDADSNYAFAGSKLGM----KTPAGRPGCNTADDKAC 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGLPAQMQSINGTLP---NLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGH
                                                                              354 AVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVTPELTIGGGVN-AMSGITSSAG-----MHAGGYATFDAMAAYRFTPKLKLQINADNIF
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                                                                                                                               AAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDI
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llarity 24.7%; Pred. No. 2.5e-25;
Conservative 126; Mismatches 341; Indels 138;
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Best Local Similarity
Matches 198; Conserv
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RESULT 22
E64817
                     A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E64817
A;Stature number: A64720; MUID:97426617; PMID:9278503
                                                              probable membrane protein b0805 - Escherichia coli (strain K-12)

(;Species: Escherichia coli

(;Species: Escherichia coli

(;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002

(;Accession: E64817

R;Blatter, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; 1

R; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.
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C;Superfamily:
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A;Experimental sour
C;Genetics:
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nucleic acid sequence
e type: DNA
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                                                                                                                                                                                                                                                                          YLRTDAAIFYK-RORFRAALNIRNLEDLKYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASNYSQFASFTIRGFNSFDQGGNNFTRNGLGYRFGS-QGT--NFSNIERIEVLRGPGSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSNDDGRSSVYARGYEY----SEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLF 160
                                                                                                                                                                                                                                                                                                          YATEDAMAAYRETPKLKLQINADNIENRHYY
                                                                                                                                                                                                                                                                                                                                                                                                                 TINDPANPEFS----IQTGEQNSRGIELNVAGEILPGWNIIAGYAYTDARI-TQDNSLPI
                                                                                                                                                                                                                                                                                                                                                                                                                                               AA--PLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNLNGRI PRNRSIGQADSTYSPEI VRVGYNLEHKFSEDWLLRNAFYYSHFYNKTRDTYFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSL----PQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYS---DRDADSNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGSGNPGGTINIVTKOPLSEPFYSVEAAIGSYDFYRGAIDLSGPLDDSKTALYR----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.6%;
ilarity 25.5%;
Conservative 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :BA000019; PIDN:BAB73874.1; strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6%; Score 475; DB 2; 15%; Pred. No. 4.9e-25; 120; Mismatches 301;
                not shown;
                                                                                                                                                                                                                                                                          838
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                translation
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                                                                                                               V.; Riley,
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RESULT AC2140

23

C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 C;Accession: AC2140

Anabaena sp. strain PCC #text\_change 30-Jun-2002

PCC

ferrichrome-iron receptor [imported] - Nostoc sp. (strain

R; Kaneko,

Nakamura,

Y.; Wolk, C.P.; Kuritz, T.;

Sasamoto,

S.; Watanabe,

A.; Iriguchi

```
A;Residues: 1-760 <BLAT>
A;Cross-references: GB.AE000182; GB:U00096; NID:gl787015; PIDN:AAC73
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor C;Keywords: transmembrane protein
F;1-49/Region: tonB-box
F;17-33/Domain: transmembrane #status predicted <TMM>
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Best Local Sim
Matches 170;
737
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                                 VGGANTENI PGSERTW--TANLRY
                                                                                                        AMSGITSSAGMHAG-----
                                                                                                                                        NITPAWQVIGGYTQQKATIKNGKDVAQDGSSSLPYTPEHAFTLWSQYQATDDISVGAGAR
                                                                                                                                                                         AVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLL--MPKHSANLWTTYQVTPELTIGGGVN
                                                                                                                                                                                                               NTSEIGTKWQVLDKRLLLTAALFRTDIENEV----EQNDDGTYSQYGKKRVEGYEISVAG
                                                                                                                                                                                                                                     NQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISG
                                                                                                                                                                                                                                                                                                                                                            AIYAFDTLQITRDFELNGGIRLDNYHTEYDSATACGGSGRGAITCPTGVAKGSPVTTVDT
                                                                                                                                                                                                                                                                                                                                                                                                GIYGKSTFHPADGLSLIGGGRLGHYKIE-----SGEG------
                                                                                                                                                                                                                                                                                                                                                                                                                                   FTRETQTN-----YGVNPVTLPAVNIYHPDSSIHPGGLTRNGANANGQT-----DTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NITOPTSDVNSWTWSRTANTK------DVSNKILTNQTNLTSTFYTGSIGHDVSTGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GMKTPAGRPG----CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPOHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNY---AFAGSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADTSNSIYIDGI----RDIGSVSRDTFNTEQVEVIKGPSGTDYGRSAPTGSINMISKQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEYS-EYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPT 178
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INKSGYRYHPGEPRTFLLTANMHF
                                                                     YI-----GSMHKGSDGAVGTPAFTEGYWVADAKLGYRVNRNLDFQLNVYNLFDTDYVAS
                                                                                                                                                                                                                                                                                      ÄKSGNLMNWKÄGÄLYHĹTENGNVYINYAVSQQPPGGNNFALAQSGSGNSÄNRTDFKPQKA
                                                                                                                                                                                                                                                                                                                       ASKTKFTGY-AGAVYDLNDNNSLYLSLSQLYTPQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDTHNFYGTDSDYDDSTTDTATMRFEHDINDNTTIRNTTRWSRVKQD---YLMTAIMGGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---YGVAPSVAFGLGTANRLYLNYLHVTQHNTPDGGIPTIGLPGYSAPSAGTAALNHSGK
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Pred. No. 9e-25;
                                                                                                        -GYATFDAMAAYRFTPKLKLQINADNIFNRHYYAR
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA. Res. B, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AC2140

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-867 <KUR>
A;Residues: 1-867 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74373.1; PID:g17131767; GSPDB:GN00179

A;Experimental source: strain PCC 7120

C;Genetics:
A;Gene: all2674

C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                                                                                     TPVIRGFESRNLLRNGLRDDSLRFQSEIANV---ERVEVLKGPASVLFGQGDLGGVVNLV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | | : : | | : : | | | : : | | | STAF-----LDVPESTTVLPIANSSTSN----GLNRDGRTLRRFLVENPSSTTSLTFNN 509
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                                                                                                                                                                                                                                                                                                         ----RGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NYAFAGSKLGMKTPAGR---PGCNTADDKACAVGL---GTEIKO-----KALAFDA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKGVRGYSHTVATENLDE--FGIYGKSTFHPADGLSLIGGGRLG----HYKIESGEGKTL 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             556 PESVSSFAIPFGNTNTEKNSLGIYAQDQISLSKNIILVLGGRLDFVNQDYEDLLSEESF 615
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                                                                                                                                                                                                                                                                                                                                                                                                                RKRP--TKAFQ-GHAAAGFGTHKQYKABADVSGSLNSDGSVRGRVMAQTVGASPRPAEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                   1: |: |: |: |: |: || 313 TKQPLNTPYYSIGYQVGQFGLH---RPTIDFSGPLDKDG-----VAYRLNAAYQTAESF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --NNRHETFYAAADWDI--NPDTVLGAG--YL-YQQRHLAPYNGLPA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 - DANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDR---DADS
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                                                                                                                                                                                                                                                       Indels 175;
                                                                                                                                                                                                                         Length 867;
                                                                                                                                                                                                                        Query Match 12.4%; Score 467.5; DB 2; Best Local Similarity 24.7%; Pred. No. 1.6e-24; Matches 186; Conservative 127; Mismatches 264;
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RESULT 24 S74450

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NiAlternate names: protein sll1406
(Species: Synechocystis sp.
A;Variety, PCC 6803
(C;Date: 25-Apr-1997 #text_change 20-Jun-2000
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A;Start codon: GTG
C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NID:g1651650; PIDN:BAA16602.1; PID:g165167
to the EMBL Data Library, June 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Keywords: iron transport
F;213-346/Domain: tonB-dependent receptor amino-terminal homology <TNN>
F;547-828/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 VLSLTSSSTAIAPENPESEIEVV-----ATQEGQGEASYFVPSASTATGLDTPLL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 ADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEF-----VIGADYNRFRSTN 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EIPOSVSIITNOOVKDRNVDTFDQLARKTPGLRVLSNDDGR-SSVYARGYEYSEYNI--- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGAD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WNKPKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLAALSSSVFAA---QTADLETVHIKGQRSYNAIVTEKNGDYSSF--AVTVGTKIPASLR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- DGLPAQ-MQSINGTLPNLPAPDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SLNSDGSVRGRVMAQTVGASPRPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------TLTWNIGPDTKLNIYGQYTTNRETLDEGIPAP---NIADLPSNRFLGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHT---VATE----NLDEFGIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----YTNTPFPIAPEFFRDDQVNRFAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKT-------KFTGYAGAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YDLNDNNSLYLSLSQLYTPQ--TNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YQPIPTVSLYGSYTTSFNPSFAASLNADGSTFDPQTGRQFEVGVKAD-ITDKLSVTFSAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 182; Conservative 119; Mismatches 303; Indels 184;
6803
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ferrichrome-iron receptor 2 - Synechocystis sp. (strain PCC N;Alternate names: protein sll1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S74450
A; Status: nucleic acid sequence not shown; translation not A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reference number: S74322; MUID:97061201; PMID:8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Cross-references: EMBL:D90899; GB:AB001339; A;Note: the nucleotide sequence was submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAAAGFGTHKQYKAEADVSG------
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|                                                                                                                                                                          | 52 NDNWKLRSAFRIVSTQTSSFVTEPGSL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                           | 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 |
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| INPDT- 248                                                                                                                                                               | 91 THKQYKAEADVSG ::   : 39 FFRPTVDFNS 49 -VLGAGYLYQQRH             96 LVFDLEYLKDSR- 07 GNGGYGKVGMRYS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 10 10 N 10 H                                                                                                                                                                                                                              | 2 2 2 2 2                               |
| ;<br>3; Gaps 25;<br>EIPOS 76<br>         <br>DIPOS 223<br>GLPAQ 133<br>                                                                                                  | Match (12.2%; Score 460.5; DB 2; Length 851 (Local Similarity 23.6%; Pred. No. 4.9e-24; ES 173; Conservative 120; Mismatches 316; Indels 12 (VLAALSSVPAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVOTKIPASLR                                                                                                                                                                                                                                                                                                                                                                                                              | Query<br>Best I<br>Matche                                                                                                                                                                                                                 | D                                       |
| strain PCC 7120 30-Jun-2002 30-Jun-2002 ; Watanabe, A.; Iriguchi v.; Yasuda, M.; Tabata, S fixing Cyanobacterium Ana fixing Cyanobacterium Ana gtor amino-terminal homol | -iron receptor [imported] - Nostoc sp. (strain PCC 712 Nostoc sp.  Nostoc sp.  toc sp. strain PCC 7120 is a synonym of Anabaena sp. s Dec-2001 #sequence_revision 14-Dec-2001 #text_change 3 : AB2129 : AB2129 : Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M. 205-213, 2001 mplete Genomic Sequence of the Filamentous Nitrogen-fi number: AB1807; MUID:21595285; PMID:11759840 : AB2129 reliminary type: DNA 1-851 <kur> 1-851 <kur> 1-851 <kur> 1-851 <kur> 2588  1y: ferrichrome-iron receptor 1; tonB-dependent recept</kur></kur></kur></kur> | RESULT 25 AE2129 AE2129 C;Species: Note C;Species: Note C;Accession: R;Kaneko, T. Nakazaki, N DNA Res. 8, A;Title: Com A;Reference A;Accession: A;Status: pr A;Molecule t A;Residues: A;Cross-refe A;Experiment C;Gene: alr2 C;Superfamil | CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA |
| DQREGDL 764 PGSERTW 714   :   PGAPFTV 820                                                                                                                                | NSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 7 616<br>0 717<br>0 665<br>7 765<br>0 765<br>0 782                                                                                                                                                                                        | D                                       |

| Db 594 DFTNOSFISIVÖVKFFDISÖQAFSRRÍGIVÖQPITPLÄÄYSÄSSÄQNEGI OY 527 LKPROGNOFEVGYKGSYMDDRLMARVSFYRMKDKNAAAPLNPNKKTRYA Db 654 IEPERGYVEVGYRGFLDGCLIASAGGOITKINVATPOPADLNES OY 654 IEPERGYVEVGYRGFLDGCLIASAGGOITKINVATPOPADLNES                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                |                                                                                                                                                                                                                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                                                                                |
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| QRDNSR 653 ALGKRV 582 : : PVGEVR 707 TYQVTP 641   :: 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 764 TYPEL 7 | 239 AADMDINPDTVLGAGXLYQORHLAPYNGLPADANNKLPS  : | Query Match  12.2%; Score 460; DB 2; Length 760;  Best Local Similarity 22.6%; Pred. No. 4.5e-24;  Matches 168; Conservative 109; Mismatches 333; Indels 134; Gaps  65 KIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGL-RVLSNDDGRSSVYARG 119 | protein ECs0883 [imported] - Escherichia coli (strain O157:H7, cherichia coli 1-2001 #sequence_revision 18-Jul-2001 #text_change 24-Aug-2001 (290739 (790739 (7) Kuhara, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K. Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. 1-22, 2001 (1-22, 2001 (1-22, 2001 (1-22, 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), 2001 (1-22), | 594 DFTNQSFLSIVÖGVKFFDISDQAFSPRIGIVYQPITPLSLYASYSRSFAQNFGIQDUSR 527 LKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRV : |

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C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A33043
C;Accession: A33043
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Ature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathora, A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE004896; GB:AE004091; NID:g9951094; PIDN:AAG08222.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable outer membrane protein PA4837 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                135 QSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYA-----AADWDIN 245
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                                                                                                          -KTLHK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 VSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRS--SVYARGYEYSEYNIDGLPAQM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.2%; Score 459; DB 2; Length 708;
Best Local Similarity 22.7%; Pred. No. 4.8e-24;
Matches 172; Conservative 135; Mismatches 329; Indels 122; Gaps
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                     391 YNRFRSTNEQGRTTLYARGGL---ALNEFRSIPQVDLIANARKGVRGYSHTVATENLDEF
                                                      400 FTRETQTN:-----YGVNPVTLPAVNIYHPDSSİHPGGLTRNGANANGQT-----DTF
                                                                                                                                                       447 AIYAFDTLQITRDFELNGGIRLDNYHTEYDSATACGGSGRGAITCPAGVAKGSPVTTVDT
                                                                                                                                                                                                    ASKTKFTGY-AGAVYDLNDNNSLYLSLSQLYTPQ------TNLDADGKLLKPRQG
                                                                                                                                                                                                                                                                                             NOPEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISG
                                                                                                                                                                                                                                                                                                                                                                                     593 AVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLL--MPKHSANLWTTYQVTPELTIGGGVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               651 AMSGITSSAGMHAG------GYATFDAMAAYRFTPKLKLQINADNIFNRHYYAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSSVFAAQT---ADLE--TVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIPQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : : ||| : : ||| : : INKSGYRYHPGEPRIFILLTANMHF 760
                                                                                                            GIYGKSTFHPADGLSLIGGGRLGHYKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      699 VGGANTFNIPGSERTW--TANLRY 720
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E85589
hypothetical protein Z1026 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: E85589
R;Perna, N.T.; Punkett III, G; Burland, V; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Reference number: A85480
A;Reference spreliminary
A;Molecule type: DNA
A;Reference: SB:AE005174; NID:912513801; PIDN:AAG55177.1; GSPDB:GN00145; UWGP:ZIG
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1026
C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 VDTHNFYGTDSDYDDSTTDTATMRFEHDINDNTTIRNTTRWSRVKQD--YLMTAIMGGAS 347
                              592
                                                                                                                                                                                                                           622
                                                                                                                                                                                                                                                                                                                                                                                              120 YEYS-EYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPT 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 NITOPISDVNSWIWSRIANIK------DVSNKILINQINLISIFYIASIGHDVSIGVE 399
                                                                                                                                                                                                                                                                        AVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLL--MPKHSANLWTTYQVTPELTIGGGVN 650
                                                                                                                                                                                                                                                                                                                                                                  651 AMSGITSSAGMHAG-----GYATFDAMAAYRFTPKLKLQINADNIFNRHYYAR 698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ADANNKLPS 277
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-- KTLHK 484
                                                                                         -----TNLDADGKLLKPRQG
                                                                                                                                 AKSGNLVNWKAGALYHLTENGNVYINYAVSQQPPGGNNFALAQSGSGNSANRTDFKPQKA
                                                                                                                                                                                                           NOFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.2%; Score 460; DB 2; Length 760; Best Local Similarity 22.6%; Pred. No. 4.5e-24; Matches 168; Conservative 109; Mismatches 333; Indels 134;
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                                                                                         ASKTKFTGY-AGAVYDLNDNNSLYLSLSQLYTPQ-
  GIYGKSTFHPADGLSLIGGGRLGHYKIE-
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| ર્ક                                         | 유 성                                                            | 유왕                                                                   | B 8                                                                 | Query<br>Best I<br>Matche                                                                                                                                      | A; Molecule A; Residues: A; Cross-ref C; Genetics: A; Gene: AGR A; Map posit                                                          | A;Title: Genda;Reference : A;Accession: A;Status: pro                                                                                                                                 | R;Goodne<br>A.; Liu<br>Science                            | C; Dat         | G97408                                                                 | ppem | 문 4 | 8          | 유 성                                                       | 유 성                                                              | В                                                                | Ş                     | 융                                                                | Ş                                                         | B &                                                       | ? { | ₹ <b>\$</b>                                                 | 밁   | Ś                                                                | В                                                        |
|---------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------------------|---------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------|----------------|------------------------------------------------------------------------|------|-----|------------|-----------------------------------------------------------|------------------------------------------------------------------|------------------------------------------------------------------|-----------------------|------------------------------------------------------------------|-----------------------------------------------------------|-----------------------------------------------------------|-----|-------------------------------------------------------------|-----|------------------------------------------------------------------|----------------------------------------------------------|
| 177                                         | 119<br>140                                                     | 80<br>80                                                             | 24 2                                                                |                                                                                                                                                                | idues: idues: ss-refe etics: e: AGR positi                                                                                            | le: (<br>erencession                                                                                                                                                                  | odner, B.<br>Liu, F.;<br>nce 294,                         | 63810<br>6:30  | prote                                                                  |      | 672 | 685        | 632<br>612                                                | 572<br>556                                                       | 496                                                              | 514                   | 436                                                              | 462                                                       | 383                                                       | . ( | 358                                                         | 292 | 298                                                              | 240                                                      |
| PTKAFQGHAAAGFGTHKQYKAEADVSGSLN-SDGSVRGR 214 | GYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKR 176 | VGTKIPASLREIPQSVSIITNQQVKDRN-VDTFDQLARKTPGLRVLSNDDGRSSVYAR 118<br> - | GQFMSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVT 61<br> | / Match 11.9%; Score 450.5; DB 2; Length 747;<br>Local Similarity 25.0%; Pred. No. 2e-23; .<br>1es 195; Conservative 104; Mismatches 358; Indels 123; Gaps 33; | type: DNA<br>1-747 <kur><br/>erences: GB:AE007869; PIDN:AAK86224.1; PID:g15155326; GSPDI<br/>C_718<br/>Ton: circular chromosome</kur> | A;Pitle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum<br>A;Reference number: A97359; PMID:11743194<br>A;Accession: G97408<br>A;Status: preliminary | <pre>; Hinkle, G.; G Wollam, C.; Al 2323-2328, 2001</pre> | on 30-Sep-2001 | ein U61401 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) |      |     |            | NLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQ 684 | XTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSA 631 | FKPNGGTDMAGKAFDPEEGRGYEAGVKLDLLDGRLGMTLAAFHLKKKNVLTADPSNPGYQ 555 | EVGYKGSYMDDRLNARVSFYR | RGLLGVRFDRYRQDMNATRLNNGRFRETSSQQTQRAATPRIGVLYQATPEVGLFANASKS 495 | SLIGGGRLGHYKIESGE-GKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQL 513 | LRSIPSRNPYAIDIRRPVYGQPKPPFGRDDRNHEEVDAMALNLQDQIEFSEKW 435 |     | GTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLA 412 | т.  | VFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGL 357 | PDTSLLVEAEVVRNRQVFDRGTVAPHNHLGSLPRSRFFGEPDDGKIDNNNET 291 |
| Ş                                           | 95<br>AG                                                       | Z E Q                                                                | > > C ;                                                             | P P P P ;                                                                                                                                                      | SCi<br>A, A<br>A, T<br>B, A                                                                                                           | C;A<br>R;W<br>era                                                                                                                                                                     | Ton<br>C;s                                                | RES<br>AI3     | Db                                                                     | Q    | B & | <b>?</b> ! | ρ φ<br>φ                                                  | D Qy                                                             | Дb                                                               | Ş                     | 망                                                                | Ş                                                         | B 2                                                       | , 5 | g Q                                                         | מם  | γQ.                                                              | Db                                                       |

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                                           AGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANL
                                                                                                                                        YLHSQIKTASNSRDDGIF-LLMPKHSANLWTTYQVTPE----LTIGGGV--NAMSGITSS
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RESULT 30 AI3197

TonB-dependent receptor [imported] - Agrobacterium tumefaciens (strain C58, Dupont) plas C;Species: Agrobacterium tumefaciens C;pate: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002 C;Accession: A13197 
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Lerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 
ster, E.W. A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W. A;Accession: A3307; PMID:11743193 
A;Accession: A31307 
A;Reference number: AB2577; PMID:11743193 
A;Recession: A3199 
A;Residues: 1-819 
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CKURP A;CKURP á 밁 Ś A;Cross-references: GB:AE008687; PIDN:AAL45999.1; PID:g17743754; GSPDB:GN00188 A;Experimental source: strain C58 (Dupont) A;Genome: plasmid ;Genetics: ;Gene: Atu5311 Query Match 11.9%; So Best Local Similarity 25.5%; Pr Matches 187; Conservative 106; 134 93 33 LETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDT 92 LQTITVQGAESAYGHV---DGIVASRSAT-GTKTDTPLIEVPQSISVITADEVKARGAET 189 11.9%; Score 450; DB 2; Length 819; 25.5%; Pred. No. 2.5e-23; tive 106; Mismatches 349; Indels 92; Gaps

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---- DIFDQLARKTPGLRVLSNDDG-RSSVYARGYEYSEYNIDGLPAQMQSINGTLPNLF 145
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  IVTEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNV-
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C;Species: Nostoc sp.
A;Note: Nostoc sp.
A;Note: Nostoc sp.
A;Note: Nostoc sp.
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AC2134
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Retaus: prelliminary
A;Accession: AC2134
A;Retaus: prelliminary
A;Molecule type: DNA
A;References: GB:BA000019; PIDN:BAB74325.1; PID:g17131719; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alize266
C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
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                                                                                                                                                                                                            357 HYQKDNGVPDYQPLPYIGTVKAGPYGAINRDFFTGEPAYNGYDRGQAVLGYEFKHQFDDV 416
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190 IKEAVNYTAGVHV-----GGSSASTRAFDNIE--IRGFAPTPLYLDGTYLPYIGDLGGSP 242
                                                                                                          QIDPYLLERIEVLKGPSSVLYGQNYPGGMINMVSKRPTDKPFNEVVAGTGT-----DGR 296
                                                                                                                                                                                                                                                                                                                                                                                                          GYGKVGMRYSDRDADSNYAFAGS--KLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SA-GMHAGGYATFDAMAAYRF---TPK---LKLQINADNIFNRHYYARVGGANTFN--IP 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 WSIRHNAKYISVDDSYRTFFSGGYVETGGVTDYTKMRRNAIDYSS------NNQVFA 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      485 ASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYM 544
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                                                                                                                                                                        VSGSLNSDGSVRGR--VMAQTVGASPRPAEK--NNRHETFYAAADWDINPDTVLGAGYL-
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llarity 24.2%; Pred. No. 3e-23;
Conservative 120; Mismatches 303; Indels 139;
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647 796 704 ferrichrome iron receptor Atu0409 [imported] - Agrobacterium tumefaciens (strain C58, Duj C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002 C;Accession: AH3626 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Giller, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell. Science 294, 2317-2323, 2001 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, II ster, E.W. Affile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8 A;Reference number: AB2577; PMID:11743193 A;Accession: AH2626 A;Residues: 1-708 «KUR» A;Cross-references: GB:AE008688; PIDN:AAL41430.1; PID:g17738752; GSPDB:GN00186 A;Experimental source: strain C58 (Dupont)

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C; Genetics:
A; Gene: Atu0409
A; Map position:
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D83081
                                 probable outer membrane receptor for iron transport PA4514 [imported] - Pseudomonas C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 14-Sep-2001 C;Accession: D83081 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J. adman, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; LOTY, S.; Olson, M.V. Mature 406, 959-964, 2000
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Complete genome sequence of Pseudomonas aeruginosa PA01, nce number: A82950; MUID:20437337; PMID:10984043
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A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-753 <STO>
A;Residues: 1-753 <STO>
A;Cross-references: GB:AE004865; GB:AE004091; NID:g9950752; PIDN:AAG07902.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA4514
C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
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DKRYFDQVYSTHMAHVAPG--RTALLGVNFHF
                                                                                                                           DGEQRVQGVELGFNGKLTEKWKVFGGYTYLDSEIRKSTVKSDEG--NKMPQTAQNNFTLW
                                                                                                                                                         LGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSAN---LW
                                                                                                                                                                                          ADISVGNNGLDPERNRNLELGTKWAFFDDALSLNAALFR-TDKTNARVASP-DVSTLQVL
                                                                                                                                                                                                                          TNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAA
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                              NRHYYARVGGANTENI - PGSERTWTANLRYSF
                                                            TTYDLLQNFTIGGGTTYVDKQYGNTANS-TYIPSYWRYDAMASYKVSKNVDLQLNVQNLT
                                                                                           TTYQVTPELTIGGG----VNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIF
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22.9%;
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Pred. No. 8.8
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probable TonB-dependent receptor PAl322 [imported] - Pseudomonas aeruginosa (strain PAO1 C; Species: Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa C; Species: Dseudomonas aeruginosa C; Jates 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 14-Sep-2001 C; Accession: A343481
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bram, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Longure 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathon A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Accession: A83481
A; Status: preliminary
A; Molecule type: DNA
A; References: GB:AE004561; GB:AE004091; NID:g9947253; PIDN:AAG04711.1; GSPDB:GN001 A; Experimental source: strain PAO1
C; Genetics:
A; Gene: PA1322
C; Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
                                                                                                                                                                                                                                                                                                                                      Gene: PA1322
Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGFGTHKOYKAEADVSGSLNSDG---SVRGRVMAQTVGASPRPAEKNNRHETFYAAADWD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 INPDTVLG-----AGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKF---K 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 MISHDVFADLKHYFGNGGYGKVGMRYSDRDAD----SNYAFAGSKLGMKTPAGRPGCNT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 ADDKA-----CAVGL-----GTEIKQKALAFDASYSRPFRLGNTANEFVIG 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 VLAALSSSVFAAQTA-----DLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASL 70
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                                                                                                                                                                                                                                                                                                                                                                                           h 11.5%; Score 432.5; DB 2; Length 732; Similarity 23.3%; Pred. No. 3.6e-22; 78; Conservative 123; Mismatches 299; Indels 165;
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C;Species: Nostoc sp.
A;Note: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 1+Dec--2001 #sequence_revision 14-Dec--2001 #text_change 30-Jun-2002
C;Accession: AE2085
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino-terminal homola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-858 «KUR»
A;Cross-references: GB:BA000019; PIDN:BAB73935.1; PID:g17131327; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 SNDDGRSS--VYARGYEYS-EYNIDGL-----PAQMQSINGTLPNLFAFDRVEVMRGP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 SKLGMKTPAGRPGCNTADDKACAVGL-GTEIKQKALAFDASYSRPFRLGNTANEFVIGAD 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLP-SLPQHVFVG-ADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAG 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAQTVGA-SPRPAEKNNRHETPYA-AADWDINPDTVLGAGYLYQQRHLAPYNGLPADANN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor
                                                                                                                                                                        (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 858;
11.2%; Score 424; DB 2; Lilarity 23.8%; Pred. No. 1.8e-21; Conservative 124; Mismatches 328;
                                                                                                                                                                        - Nostoc sp.
                                                                                                                                                                        ferrichrome-iron receptor [imported]
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Best Local Similarity
Matches 170; Conserva
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A, Status: preliminary
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: all2236
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                            629
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-696 <PAH
A;Cross-references: GE
C;Genetics:
A;Gene: STY0396
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Nature 413, 848-852, 2001
A;Authors: Parry
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C;Accession: AC0547
C;Accession: AC0547
C;James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, R;Parkhill, J.; Dougan, G.; James, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhill, R;Parkhi
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A;Accession: AC0547
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Best Local
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YAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLW
                                                         TSTSFADENGNVLEPMKGKQWEAGVKYEPLGGNSQFSAAVYRINQTNIATKEEPTDP---
                                                                                                                     TPOTNLDADGKLLKPROGNOFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTR
                                                                                                                                                                                  DRWRFTLGGRYDRVSVSNID--KLHDSRSDLDKNNVSTRAALLYLFDNGVAPYLSYSTAF
                                                                                                                                                                                                                                        DGLSLIGGGRLGHYKIESGEGKTLHKA----SKTKFTGYAGAVYDLNDNNSLYLSLSQLY
                                                                                                                                                                                                                                                                                                     NHTTGY-----YGAFPPIDAFNPVYGAQPDYITLYSREKHKLRQTGYYLQDQM-SW
                                                                                                                                                                                                                                                                                                                                                                 GRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATE -- NLDEFGIYGKSTFHPA 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQ 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FFEGEDDYDKYDRRENMVGYNIEHLFDNGWSVRQKLRYLHTKVTLNQVYAAGWLN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFVGA-DWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPA 340
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Pred. No. 2e-21;
1; Mismatches 353;
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, L.; White,
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A;Molecule type: DNA
A;Residues: 1-853 <KUR>
A;Cross references: GB:BA000019; PIDN:BAB73884.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr2185
C;Superfamily: ferrichrome-iron receptor 1; tonB-d
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C;Accession: AC2079
R;Kaneko, T.; Nakamura, Y.; Wolk, C.D.; Kuritz, T.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, N
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DNA Res. 8, 205-213, 2001
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M.; Yamada, M.; Yasuda, I
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| - Synechocystis sp. (Strain PCC 6803) slr1490 ce_revision 25-Apr-1997 #text_change 20-Jun-2000 ani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda of the genome of the unicellular cyanobacterium Synechocystis MUID:97061201; PMID:8905231 ence not shown; translation not shown ence stown; translation not shown ence was submitted to the EMBL Data Library, June 1996                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, (hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                           R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows, Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 983-988, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: C95382
                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable ferrichrome-iron receptor [imported] - Sinorhizobium meliloti (strain
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F:, Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, I
L.; Hyman, R.W.; Jones, T.
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A; Residues: 1-714 < KUR>
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                                                                    A;Genome: plasmid
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                  Score 411; DB 2;
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                                Length 714;
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                                                                                     SVWGTYTLEGDGARGDMLFGLGARYTDAYYTSITNTTSSESA--VVFDAAFTYKIQENTT
                                                                                                                              NLWITYQVIPELTIGG---
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FOLNVNNLFDEKHVASKDSGAVYYN-PG--RSILATLROSW
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RESULT 41 C81861

C91861
hypothetical protein NMA1663 [imported] - Neisseria meningitidis (strain Z2491 serogroup C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001
C;Accession: C81861
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: C81861
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-615 < CPARA
A;Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84891.1; PID:g738030
A;Experimental source: serogroup A, strain Z2491
A;Genetics:
A;Genetics:

31,

Gaps

RINMTA-ATVLAA----LSSSVFAAQTADLETVHIKGQRSYNAIVT-EKNGDYSSF---- 58

σ

10.6%; Score 402; DB 2; Length 863; ilarity 22.2%; Pred. No. 6.38-20; Conservative 127; Mismatches 335; Indels 136;

Similarity

208

118

59

-AVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA 117

266 IRGFGNQFS----DTVPILRDGFRLYGGFQGITEVSHLQQVEVLKGPSSILYGQIEPGGV 321

-RGY--EYSEYNIDGLPAQMQSIN----GTLPNLFAFDRVEVMRGPSGLFDSSGEMGGI

VNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVM-AQTVGASPRPAE

170

OPLERFAYAPIVTYAİTDÖTDÜSLAVEYINDTNPADFÖLSSFGDGVAPVPRSRVINDPSD 441 271 ANNKLPSLPOHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFA 330 IVNX-----NFISAGYN-----LEHRFNENWKLRNAFRYMSYNYDYNV--- 479 331 GSKLGMKTPAGRPGCNT--ADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIG 388

KNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGL-----

229 382 442

480 389 445

.----PAD 270

444

DEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKT-LHKASKTKFTGYA----GAVY 498 577 -RIGIYLODOVSLLENLILVAGLRYDTITONTNNLOTDFNQGGNTQOTDSAVTPRIGLLY 635

ADYNRFRSTNEQGRITLLYARGGLALN----EFRSIPQVDLIANARKGVRGYSHTVATENL RPIPEISFFSNYSOSFTPNSGIDISGNPLEPERGEGFEIGVKAELFEQOLLTTLTYFNIS 695

DLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMK

661 989 559 SNSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMH--------662 | |: :| : | : || || || || || || || PYNMANLWTTYEIQS------GALQGLGFGIGFNYVGDRFGDLANT 802

615 752 663

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ઠે g -- AGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPG

696 KNNVAVSDPVNPLFLST----IGTQQSQGIELDIVGEILPGWKIIGNYSYINAKVTEDTD 751

DKNAAA--PLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQI--KTA

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Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
           C;Keywords: iron transport
F;240-375/Domain: tonB-dependent receptor amino-terminal homology <TN
F;581-863/Domain: tonB-dependent receptor carboxyl-terminal homology
                                                                                          Matches 171;
                                                                  Query Match
Best Local
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                                       26;
                                                                                                                                      EYSEYNIDGLPAQMQSING----TLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNL 172
                                                                                                                                                                                                                                 VRKRPTKAFQGHAAAGFGTHK-QYKAEADVSGSLNSDGSVRGRVMAQTVGASP-RPAEKN 230
                                                                                                                                                                                                                                                  RVWGRKHMVYGIAEADAGDSSVLTLGGMYQKSREVPDFSGIILSCENQKTAPFSSTP--A 313
                                                                                                                                                                                                                                                                                                                                                                      366
                                                                                                                                                                                                                                                                                                                                                                                                               :|:| :| || |: || || || || || AKVGQFFLKNEHAAGLSDED--AVGFLTE-KNEVIPFEPKDKALEKLKAYRDETAKEYRE 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKDDFVKNRFDNTAFEQYRSRRAAERKAGFDECMSAPFALDFICQGSWGDPGVD----- 477
                                                                                                                       TVGTKIPASLREIPOSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGY 120
                                                                                                                                                                                                                                                                                     ---NRHETFYAAADWDINPDTVLGAGYLYQQ------RHLAPYNGLPADA 271
                                                                                                                                                                                                                                                                                                                                           NNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAG 331
                                                                                                                                                                                                                                                                                                                                                                                               SKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRL----GNTANEFVI 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                    388 GAD---YNRFRSTN-EQGRITLYARGGLALNEFRSIP-QVDLIANARKGVRGYSHTVATE 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 NLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLND 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRKATANRRYSYMPLRHTKDDRQWGIKLDLTGTYGLFGREHDFFVGY--AYGDEKIRSEY 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNSLYLSLSQLYTPQTN-----LDADGKLLKPRQGNQFEVGYKGSYMDDRLNAR- 551
                                       Gaps
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                                                                                FRINMTAATVLAALSSS-----VFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAV
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           Length 635;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEI-----SGAV 594
         / Match 10.8%; Score 407.5; DB 2; Local Similarity 24.4%; Pred. No. 1.6e-20; nes 158; Conservative 111; Mismatches 258;
         Query Match
Best Local S:
Matches 158;
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Fortichrome-iron receptor 1 - Synechocystis sp. (strain PCC 6803)

N.Alternate names: protein s111409
C.Speciae: Synechocystis sp.
A.Variety: PCC 6803
A.Variety: PCC 6803
C.Speciae: Synechocystis sp.
A.Variety: PCC 6803
C.Spate: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C.Satcession: 574447
R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A.Fitle: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis S.
A.Reference number: S74322; MUID:97061201; PMID:8905231
A.Recession: S74447
A.Status: nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: Le63 - KAN
A.Residues: Le63 - KAN
A.Roses-references: EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BAA16599.1; PID:g165167
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C.Generica:
A.Start codon: GTG
A.Start codon: GTG
RESULT 42
```

C;Species: Yerbina enterocolitica C;Dates: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 29-Sep-1999 C;Dates: 01-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 29-Sep-1999 C;Dates: 01-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 29-Sep-1999 R;Bacumler, A.J.; Hantke, K. Mol. Microbiol. 6, 1309-1321, 1992 Mol. Microbiol. 6, 1309-1321, 1992 A;Fitle: Ferrioxamine uptake in Yersinia enterocolitica: characterization of the recepto A;Accession: 822673; MUID:92349959; PMID:1640832 YTVGDYIIGNAAIFYQ-RDKYRVALNIRNFTNANYVRAVSGNQTGIEPG 850 ferrioxamine receptor precursor - Yersinia enterocolitica 803 RESULT 43 셤 ઠે

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A;Molecule type: DNA
A;Residues: 1-710 <BAE>
A;Cross-references: EMBL:X60447
C;Genetics:
RESULT 44
C83588
probable hydroxamate-type
C;Species: Pseudomonas aer
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C;Superfamily: ferrichrome-in
C;Keywords: membrane protein
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Best Local S
Matches 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolog
                                                                                                                                                                                                                                                                                                                                                                                                                      448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRPQFTSEGHERLTAGNNNTQVAAFDYTDAISEHWAFR----LTGITRNSDTMYDHQREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSEYN---IDGLPAQMQSINGTLPNL----FAFDRVEVMRGPSGLFDSSGEMGGIVNLVR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTK 65
                                                                                                   DASVRADLGTWAASLKGAFVQLNVNNIADKKYVAAC-YSTSYCYWGAERSVQATVGYDF
                                                                                                                                    DAMAAY---RFTPKLK----LQINADNIFNRHYYARVGGANTENIPGSERTWTANLRYSF
                                                                                                                                                                        NDGNTPVLAPSNMASLWAQYEA-----GYGINVGAGIRYIGKQWADDANTLRVPSYTLG
                                                                                                                                                                                                         RDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGI-----TSSAGMHAGGYATF
                                                                                                                                                                                                                                           DVANRAVP-----ATYYVPAGKVNSQGLELEARSQISDRLSVIAGYTYNRVKFKDAIDG
                                                                                                                                                                                                                                                                              D-KNAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNS
                                                                                                                                                                                                                                                                                                                DSGISPYVSYSQAITPSLFPDAQQXLLKPMTSEQYEVGIIYQPPGSTSLYSAALYDLTQN
                                                                                                                                                                                                                                                                                                                                                 NDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVG--YKGSYMDDRLNARVSFYRMK
                                                                                                                                                                                                                                                                                                                                                                                     GVYLQDEM-TLDNWHLNLSGRYDRMKTENINNTANSTDERTDNHAS-----GRASLLYSF
                                                                                                                                                                                                                                                                                                                                                                                                                      GIYGKSTFHPADGLSLIGGGRLGHYKIE-----SGEGKTLHKASKTKFTGYAGAVYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSDRTLMNRYYS---GEDSSLNAFAVDNQLEADLRTAAVKHKVLLGVDFQKFRNNLRSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDGE----SNHNVFKRWQQIYSYEFSHKFDDVWSFRQ-NASYTHSNTQLEQVYQGGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RMRLLRHYCGNPMKIPRCYCALICKKTLPAGY-----HSAVPADGSIYGQXLSRGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFYAAADWDINPDTV-----LGAGYLYQQRHLAPYNGLPADANNKLPSLPQHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRPTKAFOGHAAAGFGTHKOYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGDVNNTFLDGL--RLLSDGGSYNVLQVDPWFLERIDVIKGPSSALYGQSIPGGVVMMTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDQPLILTAQSVSVVTRQQMDDQNVATVNQALNYTPG---VFTGFSGGATRYDTVALRGFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVY----ARGYE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAFIIKRSA--ILCSLAMFIPLASIAD-DTIEVTAKAGHEADL--PTSGYTATTTKGATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATENLDEF
aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.5%;
                  ferrisiderophore
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Pred. No. 1.1e-19;
24; Mismatches 342
                  receptor PA0470 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DYLLT----TPGINTSYLSRRYEQS
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A;Cross-references: GB:AE004484; GB:AE004091; NID:g9946320; PIDN:AAG03859.1; GSPDB:GN001
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VGGANTFNIPGSERTWTANLRYSF
                                                                  VNAMSGI----TSSAGMHAGGYATFDAMAAY---RFTPKLK---LQINADNIFNRHYYAR
                                                                                                    DNLKMIGAYSYADTEVKKGQYAGNRLQQA-----
                                                                                                                                  PKWQIHAGYSYLHSQIKT---ASNSRDDGIFLLMPKHSANLWTTYQ----VTPELTIGGG
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                                   <u>ARYVGSTYGDQANTYDGYAGSYTLYDAAVRYDLGQLNGSLKGVSVAVNANNLFNKDYLAS</u>
                                                                                                                                                                        VGS--DSLFTAAV--YDLRQENVSVSQNIGGTPVTSQT----GEVKVSGIELEATSNVT
                                                                                                                                                                                                        -GSYMDDRLNARVSFYRMKDKNAAAPLN----PNNKKTRYAALGKRVMEGVETEISGAVT
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Pred. No. 1.4e-19;
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K.; Lim,
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probable ferrichrome iron receptor precursor [imported] - Escherichia coli (strain O157: C;Species: Bacherichia coli C;Species: Bacherichia coli C;Species: Bacherichia coli C;Species: Bacherichia coli C;Species: Bacherichia coli C;Species: Bacherichia coli C;Species: Bacherichia coli Bacherichia coli Bacherichia coli Bacherichia coli Bacherichia coli Bacherichia C;Accession: E9118 R;Hayasah; T.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, K.; Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Makino, Mak
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                456 HPADGLSLIGGGRLGHYKIESGEGKTLHKASKTK---FTGYAGAVYDLNDNNSLYLSLSQ
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Search completed: December 18, 2002, 06:46:04 Job time : 37.0814 secs

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| P94600<br>P96949<br>P33666<br>P44523<br>P38370<br>Q00964<br>Q07833<br>Q98140<br>Q99140<br>P29533<br>P49331                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GTFD_STRMU |
| naemophilus neisseria m escherichia haemophilus myxococcus myxococcus vibrio chol bacillus su haemophilus homo sapien bacillus ci haemophilus streptococc                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | P493:      |

## ALIGNMENTS

RESULT 1 PBUA\_PSES

PSESP

| SVYLITINQVKDRNUTFUQLARKTYGLKYLSNDUKSSVYAKTRIS EXINDGLE 13<br>  :-  :  :  :  :  :  :  :  :  :  :  :  :                       | Db 167 SVTVMTRKMLDDQNLNTIEQVMEKTPGIT                                              | u c        |
|-----------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------|------------|
| , L                                                                                                                         | 115 TVLGPATGSAM                                                                   | ) E        |
| ADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIPQ                                                                               | 16                                                                                | 0          |
| 21.9%; Score 828.5; DB 1; Length 826;<br>ty 29.9%; Pred. No. 2.8e-49;<br>ervative 129; Mismatches 303; Indels 101; Gaps 26; | Query Match  Best Local Similarity 29.9%; Pred  Matches 227; Conservative 129; Mi |            |
| 90388 MW;                                                                                                                   | SEQUENCE 826 AA; 90388 MW;                                                        | S          |
| 119 TONB BOX.<br>826 TONB C-TERMINAL BOX.                                                                                   | 110 119<br>809 826                                                                | יבי ובי    |
|                                                                                                                             | CHAIN 45 826                                                                      | 'TI'       |
| Iron transport; Transport; TonB box; Signal; Receptor.                                                                      | Outer membrane; Iron transpor                                                     | пV         |
| ; TONB_DEPENDENT_REC_1; 1.                                                                                                  | DR PROSITE; PS01156; TONE DEPENDENT REC 1; 1                                      | <b>.</b>   |
|                                                                                                                             | Pfam; PF                                                                          |            |
| 451812.1;<br>531: TonB boxC                                                                                                 |                                                                                   | <b>.</b>   |
|                                                                                                                             |                                                                                   | 20         |
| a                                                                                                                           | license                                                                           | 0.0        |
|                                                                                                                             | modified and this statement                                                       | 20         |
| as its content is in no                                                                                                     | use by non-profit instit                                                          | 0.0        |
|                                                                                                                             | between the                                                                       | 20         |
| entry is copyright. It is produced through a collaboration                                                                  | This SWISS-PI                                                                     | . 0        |
| SIMILARIII: LOCAL IO OIHBR IONB DEFENDENT RECEFIOR FROIDING.                                                                | !                                                                                 | 0.0        |
| LOCATION: Outer membrane.                                                                                                   | - :                                                                               | 2 0        |
|                                                                                                                             | PSEUDOBACTIA                                                                      |            |
| ECIFIC RECEPTOR FOR THE SIDEROPHORE FERRIC                                                                                  | -!- FUNCTION: SPECIFIC RECEPTOR                                                   | 0 2        |
| ";<br>                                                                                                                      | sp.                                                                               | ט א        |
| a ferric pseudobactin receptor gene of Pseudomonas                                                                          |                                                                                   | ×          |
| "Nucleotide sequence analysis and potential environmental                                                                   |                                                                                   | מ סכ       |
| )                                                                                                                           |                                                                                   | ט כ        |
|                                                                                                                             | SEQUENCE FROM N.A                                                                 | ×          |
|                                                                                                                             | RN [1]                                                                            | <b>z</b> ( |
| bacteria.                                                                                                                   |                                                                                   | 0          |
| (strain M114).                                                                                                              |                                                                                   | 0          |
| cin Mil4 receptor pouA precursor.                                                                                           | GN PBUA:                                                                          | ຄະ         |
| 9                                                                                                                           | 15-JUL-1999 (Rel. 38, Last annota                                                 | ם נ        |
| 32,                                                                                                                         | 01-NOV-1995 (Rel. 32, Last                                                        | <b>.</b>   |
| 32 (reated)                                                                                                                 | Q08017;<br>01-NOV-1995 (Rel 32 Created)                                           | 5 P        |
| randard; prt; 826 AA.                                                                                                       | ESP STANDARD;                                                                     | н т        |

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FADLKHQFNDDWSLKVAGVYSRNTQDMEYAFPSGAV----PVGATATNT-----LMLGSI 446
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                                                                                                                                     ADWDINPDTVLGAGYLYQQRHLAP-YNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDV 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       631 ANLWTTYQVTPEL---TIGGGVNAMSG--ITSSAG---MHAGGYATFDAMAAYRFTPKLK 682
----AQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAA 187
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                       GSSYVQADSFNS---DMAIYDRVEVLRGAAGMMKGAGGTAGGVNFVRKRGQDTAHTQLSL
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                                                                                                                                                                   336 LDFDLSPDTTLGLGFAWEDVDATPCWGGLPRYADGSDLHLKRSTCLNTAWNNQRSKRATY
                                                                                                                                                                                                      FADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLG
                                                                                                                                                                                                                                                                           TEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGL----AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE-93328663; PubMed-8335619;
Poole K., Neshat S., Krebes K., Heinrichs D.E.;
"Cloning and nucleotide sequence analysis of the ferripyoverdine
receptor gene fpvA of Pseudomonas aeruginosa.";
J. Bacteriol. 175:4597-4604(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
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                                                                   GFGTHKQYKAEADVSGSLNSDGSVRGR - - VMAQT
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Lamont I.L.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseaisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
        STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed=10984043;

MEDLINE-20437337; PubMed=10984043;

A GLOVER C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., A Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Polger K.R., Kas A., Larbig K., Lim R.M., A Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

"Complete 959-964 (2000).";

II PUNCTION: RECEPTOR FOR THE SIDEROPHORE, FERRIPYOVERDINE.

-: SUBCELLULAR LOCATION: Outer membrane.

-: SUBCELLULAR LOCATION: Outer membrane.

STARVATION CONDITIONS.

STRAVATION CONDITIONS.

-: SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AE004666, AAG05786.1; -.
PIR, A40601, A40601.
InterPro, IPR000531; TonB boxC.
Pfam, PF00593; TonB boxC. 1.
PROSITE; PS01409; TONB DEPENDENT REC 1; FALSE NEG.
PROSITE; PS01156; TONB DEPENDENT REC 2; 1.
OUter membrane; Iron transport; Transport; TonB box; Signal; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASLREIPOSVSIITNOOVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HVELGAGSWDNYRSELDVSGPLTESGNVRGRAVAAYQDKHSFMDHYERKTSVYYGILEFD 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIP 67
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FERRIPYOVERDINE RECEPTOR.
TONB C-TERMINAL BOX.
Y -> F (IN REF. 1).
MISSING (IN REF. 1).
S -> R (IN REF. 1).
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entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                  STRAIN=WCS358;
MEDLINE=91260449; PubMed=1646376;
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01-MAY-1992 (Rel. 22, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Ferric-pseudobactin 358 receptor precursor.
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                                                                                                                                                                                                                                                             Microbiol. 5:647-655(1991)
FUNCTION: SPECIFIC RECEPTOR
PSEUDOBACTIN 358.
                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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            MAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF
                                                                        DGIFLLMPKHSANLWTTYQVTPE---LTIGGGVNAMSGITSSAGMH-----AGGYATFDA
                                                                                                                                  ---PNNKKTRYAALGKRVMEGVET-----EISGAVTPKWQIHAGYSYLHSQIKTASNSRD
                                                                                                                                                                                      LSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLN
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MARYRINESLAATLNVNNIFDKKYYA-
                                                                                                        EVVPDSG----GLIASRAVDGAETKGVDVELSGEVLPGWNVFTGYS--HTRTEDADGKR-
                                                                                                                                                              ASYTDIFKPONNVDITGKPLDPEVGKNYELGWKGEFLEGRLNANIALYMVKRDNLAESTN
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L4; Conservative
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Pred. No. 4.3e-45;
4; Mismatches 306;
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TONB C-TERMINAL BOX
; 1B36164F86207951
GMAGSYGHYGAPRNATVTLRYDF
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RESULT 4

FHUE_ECOLI STANDARD; PRT; 729 AA.

ID FHUE ECOLI STANDARD; PRT; 729 AA.

AC P16859; P77292;

DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FhuE receptor precursor (Outer-membrane receptor for Fe(III)-ferrioxamine B and Fe(III)-rhodotrulic acid).

GN FHUE OR B1102.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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26;

us-09-889-267-2.rsp

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                                                                                                                                                                                                                                                                                                                           STRAIN=KI2;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=R., Haba T., Haba H., Kanai K., Kanai K., Kanai K., Kanai K., Kanai K., Kanai K., Kanai K., Kanai K., Kanai K., Kanai K., Kanai K., Kanai K., Kanai K., Kanai K., Kanai K., Kanai K., Kanai K., Maximoto K., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Satto N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           box; Signal; Receptor;
                                                                                                                                                                                         MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sauer M., Hantke K., Braun V.;
"Ferric-coprogen receptor FhuE of Escherichia coli: processing and agequence common to all TonB-dependent outer membrane receptor proteins.",
J. Bacteriol. 169:2044-2049(1987).
-!- FUNCTION: REQUIRED FOR THE UPTAKE OF IRON(III) VIA COPROGEN, FERRICAMINE B, AND RHODOTORLIC ACID.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- INDUCTION: FOR INDUCTION THE TONB AND THE EXBB PROTEIN HAVE TO
                                                                                     Sauer U., Hantke K., Braun V.;
"Sequence of the fhuE outer-membrane receptor gene of Escherichia coli K12 and properties of mutants.";
Mol. Microbiol. 4:427-437(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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Pfan, PF00593; TonB boxC; 1.

PROSITE; PS00430; TONB DEPENDENT_REC_1; 1.

PROSITE; PS01156; TONB DEPENDENT_REC_2; 1.

Outer membrane; Iron transport; Transport; TonB SIGNAL 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87194585; PubMed=3032906;
                                                           STRAIN=K12;
MEDLINE=90286919; PubMed=2162465;
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                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
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PIR; A26875; A26875.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                           SEQUENCE FROM N.A.
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                 NCBI_TaxID=562;
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122 YSEYNIDGLPAQMQS---INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPT 178
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TONB C-TERMINAL BOX.
V->P: ABOLISHES TRANSPORT ACTIVITY.
V->P: ABOLISHES TRANSPORT ACTIVITY.
G->A,V,N,D,H: IMPAIRED TRANSPORT AND GROWITH.
GROWITH.
GROWITH.
GS -> C (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 27.3%; Pred. No. 4.2e-43;
Matches 211; Conservative 148; Mismatches 308;
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01-NOV-1995 (Rel. 32, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, receptor precursor.
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P42512;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                    Complete proteome. SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U03161; AAC43213.1; -. EMBL; AE004839; AAG07609.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         opportunistic pathogen.";
Nature 406:959-964(2000).
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STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed=10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=PAO / IA602;
MEDLINE=94117363; P
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STRAIN=PAO / IA602;
                                                                                                                                                                                                                                                                                                                                                               Outer membrane; Iron transport;
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=287;
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: HIGH-AFFINITY OUTER MEMBRANE RECEPTOR REQUIRED TRANSPORT OF FE(III)-PYOCHELIN.
SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                   LSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLRE
                                                                                                                                      IPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNIDGLPA 132
DRYRAEVDVGGPLSASGNVRGRAVA---AYEDRDYFYDVADQGTR--LLYGVTEFDLSPD
                                                                         KQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRP----AEKNNRHETFYAAADWDINPD
                                                                                                               LPQSASVIDHERLEQQNLFSLDEAMQQATGVTVQPFQLLTTAYYVRGFKVDSFELDGVPA
                                                                                                                                                                       LALSPLAAAVADARKDGETELPDMVISGE---STSATQPPG-----VTTLGKVPLKPRE
                                                                                                                                                                                                                               200;
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                                                                                                                                                                                                                                                                                                                                                            PS00430; TONB DEPENDENT REC 1; FAI
PS01156; TONB DEPENDENT REC 2; 1.
mbrane; Iron transport; Transport;
                                                                                                                                                                                                                                                                                        703
720 AA;
                                                                                                                                                                                                                                Conservative
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720 T
79992 MW;
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27.2%;
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                                                                                                                                                                                                                                              Score 715.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                     FE(III)-PYOCHELIN RECEPTOR TONB C-TERMINAL BOX.
DA796313116E0CC2 CRC64;
                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                            Signal; Receptor;
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01-OCT-1994 (Rel.
01-NOV-1995 (Rel.
                                                                                                                                                                                                                                                                                  MEDLINE=93316856; PubMed=8392140;
Koster M., van de Vossenberg J., Leon
"Identification and characterization
                                                                                                                                                                                                                                                                                                                                          STRAIN=WCS358;
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-996 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation precurso
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                                                                                                                 FUNCTION: SPECIFIC RECEPTOR FOR THE SIDEROPHORES PSEUDOBACTIN BNB AND FERRIC PSEUDOBACTIN BN7, IRO MOLECULES THAT ALLOW THE ORGANISM TO EXTRACT IRON ENVIRONMENT, SPECIALLY UNDER IRON-RESTRICTED COND SUNCELLULAR LOCATION: OUter membrane.

INDUCTION: BY IRON LIMITATION IN ADDITION TO THE INDUCTION: BY IRON LIMITATION IN ADDITION TO THE OF THE TWO COGNATE PSEUDOBACTINS BNB OR BN7.
                                                                                                   SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS
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                                                                                                                   FERRIC-PSEUDOBACTIN BN7/BN8 RECEPTOR
                                                                                                                                                                                                                                                                                                         SSVYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNL
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                                                                                                                                                                      Query Match
18.8*; Score 708.5; DB 1; Length 809;
Best Local Similarity 25.7*; Pred. No. 4.8e-41;
Matches 197; Conservative 154; Mismatches 314; Indels 101;
                                        PIR; $32899; $32899.
InterPro; PR000531; TonB boxC.
Pfam; PF00593; TonB boxC; 1.
PROSITE; PS00430; TONB DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Iron transport; Transport; Signal; Receptor.
SIGNAL
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                                                                                                                                                  0B339F6E788A8C0D CRC64;
                                                                                                                             POLY-SER.
TONB C-TERMINAL BOX
           send an email to license@isb-sib.ch)
                                                                                                                                                   809 AA; 88389 MW;
                              EMBL; X73598; CAA51995.1;
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PROSITE; PS01156; TONB_DEPENDENT_REC_2; FALSE_NEG.
Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor;
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Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
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IDBNITPICATION BY MASS SPECTROMETRY, AND PUTATIVE FUNCTION.
IDENTINE-20267815; PubMed=10806384;
MOLIOY M.P., Herbert B.R., Slade M.B., Rabilloud T., Nouwens A.S.,
Williams K.L., Gooley A.A.;
"Proteomic analysis of the Escherichia coli outer membrane.";
Bur. J. Blochem. 267:2871-2881 (2000).
-i- FUNCTION: PROBABLE RECEPTOR, TONB-DEPENDENT, THAT PARTICIPATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burland V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLE TONB-DEPENDENT RECEPTOR YBIL.
TONB C-TERMINAL BOX.
1866B9C2EF68C7CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yano M., Horiuchi T.;

"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";

DNA Res. 3:137-155(1996).
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-!- SUBCELLULAR LOCATION: Outer membrane (Potential).
-!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
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Pred. No. 1.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12.";
                                                                                                                     15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable tonB-dependent receptor ybiL precursor.
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EMBL; D90718; BAA35476.1; -.
EcoGene; EG13317; ybiL.
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Best Local Similarity
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15-DEC-1998
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SEQUENCE FROM N.A.
STRAINSLT2 / SGSC1412 / ATCC 700720;
MEDLINE=215.34948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spiet
                                                                                                                                                                                    Q56145;
01-NOV-1997
                                                                                                                 Salmonella typhimurium
                                                                                                                             FOXA OR STM036
                                                                                                                                                         15-JUN-2002
15-JUN-2002
                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                   FOXA
                                                                     NCBI_TaxID=602;
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                                                                                                                                                                                                                                                                                                                                            YI-----GSMHKGSDGAVGTPAFTEGYWVADAKLGYRVNRNLDFQLNVYNLFDTDYVAS
                                                                                                                                                                                                                                                                                                                                                                                                    NITPAWQVIGGYTQQKATIKNGKDVAQDGSSSLPYTPEHAFTLWSQYQATDDISVGAGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTSEIGTKWQVLDKRLLLTAALFRTDIENEV----EQNDDGTYSQYGKKRVEGYEISVAG
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                          receptor
                                                                                                                                                                                                                 STANDARD;
                                                                                                                                          precursor.
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 Spieth J.,
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  Clifton
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 S.W.,
  Latreille
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Matches 176;
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-!- FUNCTION: FERRIOXAMINE BINDING AND UPTAKE, IN TONB PROTEIN (BY SIMILARITY). MAY PLAY A ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000531; TonB boxC:
PROSITE; PS00430; TONB DEPENDENT REC 1; FALSE NEG PROSITE; PS01156; TONB DEPENDENT REC 2; FALSE NEG Signal; Receptor; Transmembrane; Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                       StyGene; SG10646; foxA.
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB008712; AAL19318.1; -.
EMBL; AP060876; AAC15464.1; -.
EMBL; U62282; AAA04552.1; -.
HSSP; P06971; 1BY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstate the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95370139; PubMed-7642488;
Tsolis R.M., Baumler A.J., Stojiljkovic I., Heffron F., Fur regulon of Salmonella typhimurium: identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-244
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[3]
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Kingsley R.A., Reissbrodt R., Rabsch W., Ketle
Everest P., Dougan G., Baeumler A.J., Roberts
"Ferrioxamine-mediated iron(III) utilization b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SL1344;
                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                      SIGNAL
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SUBCELLULAR LOCATION: Outer membrane.
SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS
                                                                           VGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSS----VYA 117
                                                                                                                                   MSVFRINMTAATVLAALSSS---VFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVT
{\tt RGFSDGSLDNVYLDGLKMMGDTNSHSSLVVDPWFLEDIEVVRGPASVLYGRSSPGGIVAL
                        RGYEYSEYN---IDGLP--AQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNL
                                                                                                         MFMFATTRMALLIGGAIGGATFPLFAQETTKNDTV------IVT-----SPVQS
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                                                                                                                                                               Conservative 119;
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G -> R (IN REF 2).
F -> S (IN REF 2).
A -> P (IN REF 2).
HRLLVGI -> SSSAGGD ()
                                                                                                                                                                             Score 423; DB 1;
Pred. No. 1.6e-21;
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                                                                                                                                                                  Mismatches
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IN REF. 2)
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., Williams P.
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                                                    VYSNOIGASNRFDYIVL
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Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: FERRIOXAMINE BINDING AND UPTAKE, IN ASSOCIATION WITH THE
                                                                                                                                                                                                            511
                                                                                                                                                                                                                                                     571
                                                                                                                                                                                                                                                                 631
                                                                                                                                                                                                                                                                                                          -----AGYLYQQRHLAPYNGLPADANNKLPSL 278
                                                                                               SNTFFEGEDDYDKYDRRENMVGYNIEHLFDNGWSVRQKLRYLHTKVTLNQVYAAGWLN-- 333
                                                                                                                                                                    NEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATE--NLDEFGIYGKSTF 455
                                                                                                                                                                                       DRSNHTTGY-----YGAFPPIDAFNPVYGAQPDYITLYSREKHKLRQTGYYLQDQM 428
                                                                                                                                                                                                                                 -SWDRWRFTLGGRYDRVSVSNID--KLHDSRSDLDKNNVSTRAALLYLFDNGVAPYLSYS 485
                                                                                                                                                                                                                                                                                                                                       681
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VRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNR 232
                                                                                 PQHVFVGA-DWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMK 337
                                                                                                                          TPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRST 397
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Ferrioxamine uptake in Yersinia enterocolitica: characterization
the receptor protein FoxA.";
Mol. Microbiol. 6:1309-1321(1992).
                                                       HPADGLSLIGGGRLGHYKIESGEGKTLHKA----SKTKFTGYAGAVYDLNDNNSLYLSLS
                                                                                                                                                                                                                                                   QLYTPQTNLDADGKLLKPROGNQFBVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNK
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                                                                                                                                                                                                                                                                                              KTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSA
                                                                                                                                              -----ETALNRGYS----GSGEKMSAIALDNQLDGSVDTGAINHRLLVGIDYQ----
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STRAIN=ATCC 51872 / WA-C / Serotype O:8;
MEDLINE=92349959; PubMed=1640832;
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STRAIN=ATCC 51872 / WA-C / Serotype 0:8;
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ 30, 233 HETFYAAAD---WDINPDTVL-----GAGYLYQQRHLAPYNGLPADANNKLPSLP 279 122 YSEYN---IDGLPAQMQSINGTLPNL----FAFDRVEVMRGPSGLFDSSGEMGGIVNLVR 174 66 IPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVY----ARGYE 121 139; Gaps SVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTK 3 SAFIIKRSA--ILCSLAMFIPLASIAD-DTIEVTAKAGHEADL--PTSGYTATTTKGATK 58 TDQPLILTAQSVSVVTRQQMDDQNVATVNQALNYTPG--VFTGFSGGATRYDTVALRGFH GGDVNNTFLDGL---RLLSDGGSYNVLQVDPWFLERIDVIKGPSSALYGQSIPGGVVMMTS KRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEK--NNR HSSP; P06971; 1QJQ.
InterPro; IPR00531; TonB\_boxC.
Pfam; PR00593; TonB\_boxC, 1.
PROSITE; PS00430; TONB\_DEPENDENT\_REC\_1; 1.
PROSITE; PS01156; TONB\_DEPENDENT\_REC\_2; 1.
Signal; Receptor; Transmembrane; Outer membrane; Iron transport; Length 710; Indels 82EB6EC1546900B8 CRC64; POTENTIAL. FERRIOXAMINE RECEPTOR 10.6%; Score 401.5; DB 1; llarity 23.3%; Pred. No. 5e-20; Conservative 127; Mismatches 334; C-TERMINAL POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL.
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POTENTIAL. or send an email to license@isb-sib.ch) POTENTIAL. POTENTIAL. POTENTIAL POTENTIAL POTENTIAL POTENTIAL POTENTIAL POTENTI POTENTI POTENTI TONB 78382 MW; EMBL; X60447; CAA42975.1; 3317 3317 3318 3318 4318 484 499 632 S22673; S22673. fransport; TonB box. 684 702 710 AA; Query Match Best Local Similarity Matches 182; Conserv 27 28 693 65 65 427 TRANSMEM TRANSMEM TRANSMEM SEQUENCE TRANSMEM TRANSMEM FRANSMEN **FRANSMEN** FRANSMEN FRANSMEN FRANSMEN **TRANSMEM** FRANSMEM FRANSMEM FRANSMEM FRANSMEN **TRANSMEM** FRANSMEM FRANSMEM FRANSMEM *FRANSMEM FRANSMEM* FRANSMEM **TRANSMEM FRANSMEM** TRANSMEM TRANSMEM **TRANSMEM** FRANSMEM **FRANSMEN FRANSMEN** SIGNAL 116 175 174 ø

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01-APR-1988 (Rel. 07, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update
Ferrichrome-iron receptor precursor (Ferric
                                            SEQUENCE FROM N.A.
STRAIN-K12 / W3110;
MEDLINE=94261430; PubMed=8202364;
FUJITA N., MOTI H., Yura T., Ishihama A.;
"Systematic sequencing of the Escherichia coli
the 2.4-4.1 min (110,917-193,643 bp) region.";
 STRAIN=K12
                                                                                                                                                     Coulton J.W., Mason P., Cameron D.R., C"Protein fusions of beta-galactosidase receptor of Escherichia coli K-12.";
             SEQUENCE
                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                           Bacteria;
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                                       Acids
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             FROM
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/ MG1655;
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"Crystal structure of the antibiotic albomycin in complex with outer membrane transporter Fhua.";
Protein Sci. 9:956-963 (2000).
-i- FUNCTION: THIS RECEPTOR BINDS THE FERRICHROME-IRON LIGAND.
INTERACTS WITH THE TONB PROTEIN, WHICH IS RESPONSIBLE FOR E COUPLING OF THE FERRICHROME-PROMOTED IRON TRANSPORT SYSTEM.
AS A RECEPTOR FOR BACTERIOPHAGE TS AS WELL AS T1, PHISO AND COLICIN M. BINDING OF TS TRIGGERS THE OPENING OF A HIGH CONDUCTANCE ION CHANNEL. CAN ALSO TRANSPORT THE ANTIBIOTIC
                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS)
MEDLINE=20306978; PubMed=10850805;
Ferguson A.D., Braun V., Fiedler H.-P.
                                                                                                                                                                                                                                                                                                   "Transmembrane signaling across the ligand-gated crystal structures of free and ferrichrome-bound allosteric changes.";
                                                                                                                                                                                                                                                                                                                                                                                                                     "Siderophore-mediated iron transport: bound lipopolysaccharide."; Science 282:2215-2220(1998).
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Davis K., Federspiel N., Hyman R., I
Lashkari D., Lew H., Lin D., Namath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                               Locher K.P., Rees B., Koebnik R., Mitschler A., Rosenbusch J.P., Moras D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonhivers M., Ghazi A., Boulanger P., Letellier L.; "FhuA, a transporter of the Escherichia coli outer membrane, converted into a channel upon binding of bacteriophage T5."; EMBO J. 15:1850-1856(1996).
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Mol. Gen. Genet. 209:49-55(1987).
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MEDLINE=99081293; PubMed=9865695;
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MEDLINE=99074366; PubMed=9856937;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Energy-coupled transport through the outer membrane of Escherichia coli small deletions in the gating loop convert the FhuA transport protein into a diffusion channel.";
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Science 277:1453-1474(1997).
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                         SUBUNIT: MONOMER.
SUBCELLULAR LOCATION:
SIMILARITY: LOCAL TO (
   SWISS-PROT
                                                                                                                                                                                                                                                                                        95:771-778(1998).
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                              box; Signal;
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Pfam; PF00593; TonB boxc; 1.
PROSITE; PS00430; TONB DEPENDENT REC_1; 1.
PROSITE; PS01156; TONE DEPENDENT REC_2; 1.
Outer membrane; Iron transport; Transport; TonB box; Sign Phage recognition; Receptor; Transmembrane; 3D-structure;
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EMBL, W70214; AAB08580.1; --
EMBL, X05810; CAA29253.1; --
FIR, A25196; QRECFE.
FIR, S45219; S45219.
FDB, 1BY7; 13-JAN-99.
FDB, 1BY7; 13-JAN-99.
FDB; 1ECP; 13-JAN-99.
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"Analysis of the Ervinia chrysanthemi ferrichrysobactin receptor gene: resemblance to the Escherichia coli fepA-fes bidirectional promoter region and homology with hydroxamate receptors.";

J. Bacteriol. 178:1227-1231(1996).

-!- FUNCTION: INVOLVED IN THE INITIAL STEP OF IRON UPTAKE BY BINICHTSOBACTIN, AN IRON CHELATIN SIDEROPHORE THAT ALLOWS THE BACTERIA TO EXTRACT IRON FROM THE ENVIRONMENT.
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Pfam; PF00593; TonB_boxC; 1.

PROSITE; PS001156; TONB_DEPENDENT_REC_2; FALSE_NEG.

PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.

Signal; Receptox; Transmembrane; Outer membrane; Iron transport;
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01-NOV-1997 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Outer membrane. SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
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                                       --DWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG
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CNTA----DDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQ 400
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"The pesticin receptor of Yersinia enterocolitica: a novel virulence factor with dual function.";
                                                                                                                                                                                                                                                                                                                       TSFEPNLDSGAPGTPAFKPTTGEQKEVGVKFQPKGSNTLLTVSLFDITQKN----ITSYN
                                                                                                                                         ---TLEKKMWLDRNNDYSFNWANPTYNV----SVNDSMLTELSTNERNKLNQVGVYLQD
                                                                                               GRITLYARGGLALNEFRSIPOVDLIANARKGVRGYSHTVATE------NLDEFGIYGKS
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                                          358 TDİTILRRPQK------EÈNEISEFAIDNQLKATFATGSVNHTVLSGLDYKWL----
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STRAIN=1223-75-1, 8081, YE737, and 1209-79;
RAKIN A., Heesemann J.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR THE BACTERIOCIN PESTICIN AND FOR THE SIDEROPHORE YERSINIABACTIN.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F----TPKLK---LQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF
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01-NOV-1995 (Rel. 32, Last sequence update)
06-CCT-2010 (Rel. 40, Last annotation update)
Pesticin receptor precursor (IRPC) (IPR65).
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STRAIN-ATCC 51871 / WA-314 / Sero
MEDLINE-95075311; PubMed-7984105;
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8.0%; Score 303; DB 1; Length 673;
Best Local Similarity 20.9%; Pred. No. 2.7e-13;
Matches 159; Conservative 98; Mismatches 298; Indels 204;
| Refam; PF00531; TonB_boxC. | PALSE_NEG. | PF60539; TonB_boxC. | PF60539; TonB_boxC. | PROSITE; PS00430; TonB_boxC. | PROSITE; PS00430; TonB_DEPENDENT_REC_1; FALSE_NEG. | PROSITE; PS004156; TonB_DEPENDENT_REC_2; FALSE_NEG. | PROSITE; PS004156; TonB_DEPENDENT_REC_2; PALSE_NEG. | PROSITE; PS004156; TonB_DEPENDENT_REC_2; PALSE_NEG. | PROSITE; PS004156; TonB_DEPENDENT_REC_2; PALSE_NEG. | PROSITE | PESTICIN RECEPTOR. | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE | PROSITE
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Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague.", Nature 413:523-527(2001).
InterPro; IPR000531; TONB_boxC.

Pfam; PF00593; TONB boxC; 1.

PROSITE; PS00430; TONB DEPENDENT REC 1; FALSE NEG.

PROSITE; PS01156; TONB DEPENDENT REC 2; FALSE NEG.

Signal; Receptor; Transmembrane; Outer membrane; Interproteome.

Transport; TonB box; Complete proteome.

SIGNAL 22 POTENTIAL.

CHAIN 23 673 PESTICIN RECEPTOR.
                                                                                                    EMBL; Z35104; CAA84487.1; -.
EMBL; U09530; AAA69906.1; -.
EMBL; AL031866; CAA21395.1; -.
EMBL; AJ414150; CAC90722.1; -.
HSSP; P05825; 1FEP.
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                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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"Analysis of the pesticin receptor from Yersinia iron-deficient growth and possible regulation by J. Bacteriol: 177:1824-1833(1995).
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Bacteria; Proteobacteria;
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SUBCELLULAR LOCATION: Outer membrane.
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                                                       SEQUENCE FROM N.A.
MEDIATRE=81213100; PubMed=2644220;
MEDIATRE=81213100; V.;
Mau C.D., Konisky J.;
"Evolutionary relationship between the TonB-dependent outer membrane transport proteins: nucleotide and amino acid sequences of the Escherichia coli colicia I receptor gene.";
J. Bacteriol. 171:1041-1047(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-59 FROM N.A., AND SEQUENCE OF 26-46.
MEDLINE=88058737; PubMed=3316180;
Griggs D.W., Tharp B.B., Konisky J.;
"Cloning and promoter identification of the iron-regulated cir gene of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIDSALZ / MG165,
STRAIDSALZ / MG165,
BHBDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=K12 / BHB2600;
Richterich P., Lakey N., Gryan G., Jaehn L., Mintz L., Robison K.,
Church G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90264362; PubMed=2160948; Griggs D.W., Kafka K., Nau C.D., Konisky J.; Activation of expression of the Escherichia coli cir gene by an iron independent regulatory mechanism involving cyclic AMP-cyclic
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMP receptor protein complex.";
J. Bacteriol. 172:3529-3533(1990).
-!- FUNCTION: NOT YET KNOWN. POSTULATED TO PARTICIPATE IN IRON
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- INDUCTION: BY IRON AND BY A CYCLIC AMP RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                             Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
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Steffes C., Ellis J., Wu J., Rosen B.P.;
"The lyst gene encodes the lysine-specific permease.";
J. Bacteriol. 174:3242-3249(1992).
                                                                                                                                                                         ŘEVISIONS.
Nau C.D., Konisky J.;
J. Bacteriol. 171:4530-4530(1989).
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EMBL; J00007; AAA66531.1; -.
EMBL; AE000304; AAC75216.1; -.
EMBL; M19225; AAA23581.1; -.
EMBL; M89774; AAA17054.1; -.
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                         NCBI_TaxID=562;
                Escherichia.
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PROSITE; PSO0430; TONB DEPENDENT REC 1; 1.
PROSITE; PSO1156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------FAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRP 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 FRLGNTANEFV-IGADY-----NRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLI 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 L---TAINQFLTVGGEWRHDKLSDAVNLTGGTSSKTSASQYAL--FVEDEWRIFEPLALT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426 ANARKGVRGYSHTVATENLDEFGIYGKS-----TFHPADGLSLIGGGRLGHYKIESGE 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNQFEVG--YKGS-----YMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYA 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 HNGRWDYGTSELKYYGEKVENKNP------GNSSPITSESNTVDGKYTLP 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       479 GKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKL-----LKPRQ 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 WATAFKAP-------SLLQLSPDWTSNSCRGACKIVGSPDLKPET 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                               7.1%; Score 267; DB 1; Length 663;
llarity 20.6%; Pred. No. 7.9e-11;
Conservative 108; Mismatches 237; Indels 240; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAE
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                                                                                                                                                                                                                                                                    COLICIN I RECEPTOR.

TONB BOX.

TONB C-TERMINAL BOX.
S - D (IN REF. 6).
I -> N (IN REF. 1).
W, 2C68A45D4B5EE414 CRC64;
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                                                                     EcoGene; EG10155; cirA.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PIR; S24561; S24561.
HSSP; P05825; IFEP.
ECO2DBASE; B068.1; 6TH EDITION.
                                                                                                                                                                                                                                                                                                                                                                         528 I
73895 MW;
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CONFLICT
SEQUENCE
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Best Local S
Matches 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong GK.-S., Wu Z., Paulsen I.T.,
Reizer J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                             SEQUENCE
                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              opportunistic pathogen.";
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STRAIN=ATCC 15692 /
MEDLINE=20437337; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dean C.R., Poole K.; "Cloning and characterization of the ferr gene (pfeA) of Pseudomonas aeruginosa."; J. Bacteriol. 175:317-324(1993).
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                                                                                                                                                            Complete
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HSSP; P05825; 1FEP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 406:959-964 (2000)
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01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                     Pfam; PR000531; TonB_boxC.

Pfam; PR00593; TonB_boxC; 1.

PROSITE; PS00430; TÖNB_DEPENDENT_REC_1; PAI

PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.

Outer membrane; Iron transport; Transport;
SUBCELLULAR LOCATION: Outer membrane.
INDUCTION: BY IRON AND ENTEROBACTIN.
SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: SPECIFIC RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENTEROBACTIN.
                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collabeen the Swiss Institute of Bioinformatics and the EMBL outset European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in field and this statement is not removed. Usage by and for complete the statement is not removed.
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FERRIC ENTEROBACTIN F
TONB BOX.
TONB C-TERMINAL BOX.
                                   Score 256.5; DB 1;
Pred. No. 4.9e-10;
7; Mismatches 321;
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                                       Indels 209;
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15-JUN-2002
15-JUN-2002
15-JUN-2002
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                                                                                                                                     DKRLF-RAGNAQGVVGIDGAGAATYNEPG--RTFYTSLTASF
                                                                                                                                                                                                SLQATVTWYGKQKPKKYDYHGDRVTGŚANDQLSPYAIAGLGGTYRLSKNLSLGAGVDNLF
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                                                          STANDARD;
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SEQUENCE FROM N.A.
STRAIN=Rd / KW20 /
MEDLINE=95350630; P
Fleischmann R.D., A
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NCBI\_TaxID=727;
[1]

Adams M.D., White O., PubMed=7542800; ATCC 51907

Clayton

R.A.,

Kirkness

Bacteria; Haemophilus

Proteobacteria;

gamma

subdivision; Pasteurellaceae;

influenzae tonB-dependent

Hypothetical HI1466.1.

(Rel. (Rel. (Rel.

41, Created)
41, Last sequence update)
41, Last annotation updat

nnotation update)

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anguillarum (Listonella anguillarum).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                     "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435 YSHTVATE------NLDEFGIYGKSTFHPADGLSLIGGGRLGHY-----K 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474 IESG-----EGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTN--LDADGKL 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 IRSGYLAQKDGKLLYQ-----LGSVYKFTPNIATFFNHAESFRPQNNRTLIINGE- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGV 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETEISGAVTPKWQIHAGYSYLHSQIKTASNSRD-----DGIFLLMPKHSANLWTTYQ 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFDLNGQLTDNLSIAANYTY--TKVKNLENHNNKLAVGKQLSGV----PKHQASLFLAYN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTP----ELTIGGGVNAMSGITSSACMHAGGY----ATFDAMAAYRFT---PKLKLQIN 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 IGEFDFGNIRVGGGARYLGSWYAYNNTYTKAYKLPQAIVYDTFIAYDTKISGKKVSFQLN 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Soctt J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Ruhrmann J.L., Geoghagen N.S.M., Gnehm C.L., mcDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                               White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D., Peterson J., Halckey E., Dodson R., Gwinn M., Submitted (MAY-1998) to the EMEL/GenBank/DDBJ databases.
-:- SIMILARITY: LOCAL TO OTHER TONS-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000531; TonB boxC.

Pfam; PF00593; TonB boxC; 1.

PROSITE; PS01156; TONB DEPENDENT REC 2; FALSE NEG.

Hypothetical protein; Receptor; TonB box; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82; Conservative 58; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 AA; 38744 MW; BAF83C55FCC9CB2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                687 ADNIFNRHYY-ARVGGANTFNIP---GSERTWTANLRYSF 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-TERMINAL BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 5.9%; Score 221.5; DB 1
Local Similarity 24.1%; Pred. No. 4.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 GKNLSNKVYSPSTSGNASRTLIPVALGYAREVILNTKIEF
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AC P10461; P19830;
DT 01-0CT-1989 (Rel. 12, Created)
DT 01-0CT-1989 (Rel. 12, Last sequence update)
DT 16-0CT-2001 (Rel. 40, Last annotation update)
DF FATA.

GN FATA.

GN FATA.
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                                                                                                                                                    Science 269:496-512(1995)
                                                                                                                                                                                  REVISIONS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Listonella
                                                                                                                                                                                                                                                                                                                                  66 IPASLREIPQSVSIITNQQVKDRNV-DTFDQLARKTPGLRVLSNDDG--RSSVYARGY-- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYSEYNIDGL----PAQMQSINGTLPNLFAFDRVEVMRGPSGLFDS---SGEMGGIVNLV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 DIGDVMFNGLYGIAPYYRSS-----PEM--YQRIDVLKGPASLLNGMPPNGSVGGSINLV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 TKRAQEAPITSFTGTYMSDSQFGGHIDIGRRFGENEQFGVRFNGVFRDGDASVDGQSRKA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLAS-------LSLDWRNDIALIEADLYFSTERVDGPNRGLSIASGVD 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 137; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 RINMTAATVLAALS---SSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIALLVALQISASALPISITHAEEQAD-ESITVYGQAN-EAYAAGKISKASSIGM-LGDK 78
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                                                                                                                                                            Actis L.A., Tolmasky M.E., Farrell D.H., Crosa J.H.; "Genetic and molecular characterization of essential components c
the Vibrio anguillarum plasmid-mediated iron-transport system."; J. Biol. Chem. 263:2853-2860(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Signal; Receptor; Transmembrane; Outer membrane; Iron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 726;
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FERRIC ANGUIBACTIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88B67A219395B154 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 115; Mismatches 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TONB C-TERMINAL BOX
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21.6%; Pred. No. 3.1
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                                                                                                                                              MEDLINE=88139336; PubMed=2830268;
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                                                                                                                                                                                                                                                                                                             SEQUENCE OF 637-726 FROM N.A.
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EMBL; M14504; AAA79859.1; -.
PIR; B29928; B29928.
PIR; PQ0051; PQ0051.
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726
56
726
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                                                                                       FROM N.A.
                          NCBI_TaxID=55601;
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SEQUENCE FROM N.A.

SERAIN=El Tor N16961 / Serotype O1;

SERAIN=El Tor N16961 / Serotype O1;

SERAIN=El Tor N16961 / Serotype O1;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eiseen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.

Dedson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Dodson R.J., Welson K.E., Read T.D., Tettelin H., Richardson D.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Seller

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White

McDonald L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P27772; Q9KUPO;
01-AUG-1992 (Rel
16-OCT-2001 (Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Payne S.M., Calderwood S.B.; "Characterization of a Vibrio cholerae virulence factor homologous the family of TonB-dependent proteins."; Mol. Microbiol. 6:2407-2418(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Classical Ogawa 395 / ATCC 39541 / MEDLINE=93023868; PubMed=1406279; Goldberg M.B., Boyko S.A., Butterton J.R.,
SEQUENCE OF 1-151 FROM N.A.
STRAIN-Classical Ogawa 395 / ATCC 39541 /
MEDLINE-91072235; PubMed-2174861;
Goldberg M.B., Boyko S.A., Calderwood S.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=666;
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                                                                                                                                                                   "DNA sequence of both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae
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IRGA OR VC0475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                )1-AUG-1992 (Rel. 23, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TASNSRDDG-IFLLMPKHSANL---WTTYQVTPELTIGGGVNAMSG--ITSSAGMHAGGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y--FREDKNDSPTGNNNPGSWNPNIYNPVWGPEDSTYDN----YYELPVDSTQISFG
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J. Bacteriol. 172:6863-6870(1990).
-I- FUNCTION: INVOLVED IN THE INITIAL STEP OF IRON UPTAKE BY BINDING FERRIC VIBRIOBACTIN, AN IRON CHELATIN SIDEROPHORE THAT ALLOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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SIGNAL 1 25 POTENTI
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PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Virulence; Outer membrane; Iron transport; Transport; TonB
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Pfam; PF00593; TonB_boxC; 1.
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TIGR; VC0475; -.
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PIR; S25265; S25265.
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SUBCELLULAR LOCATION: OUTEY membrane.
MISCELLANEOUS: REGULATION OF THE IRGA EXPRESSION IS NEGATIVE
REGULATED AT THE TRANSCRIPTIONAL LEVEL BY IRON.
SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
GVEGKHESLE--
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                                                                                 HYFGNGGYGKVGMRYSDRDADS-----NYAFAGSKLGMKTPAGRPGCNTADDKACAVGL
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                       374 LAEQFRLTFGGR------LDHDKNYG-SHFSPRVYGVWNLDPLWTVKGG--- 415
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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TONB C-TERMINAL BOX.
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                                                                                                                                                                Escherichia coli.
Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
Escherichia.
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InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; FALSE_NEG.
Hypothetical protein; Outer membrane; Receptor; Signal; TonB b
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable tonB-dependent receptor yncD precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 -RPGCNTADDKACAVGLG-TEIKOKALAFDASYSRPFRLGN--TANBFVIGADYNRFRST 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 568 WTWLDATYRSNVCNEQDCNGNRMPGIARNMGF------ASIGYVPEDGWYA 612
Ouery Match 5.7%; Score 214; DB 1; Length 700;
Best Local Similarity 20.0%; Pred. No. 3.8e-07;
Matches 156; Conservative 114; Mismatches 317; Indels 192; Gaps
                                                                                                                                                              ------DEQTMIVSAAP 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | | | : | | | GTEARYMGDIMADDENTAKAPSYTLVGLFTGYKYNYHNLTVDLFGRVDNLFDKEYVGSV 671
                                                                                                           5 MSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGT 64
                                                                                                                                                                                                                                                  GRSSVYARGYEYSEYNIDGLPAQMQSINGTLPN--LFAFDRVEVMRGP-SGLFDSSGEMG
                                                                                                                                                                                                                                                                                                                                                   94 GSRSTY--GIRGIRLYVDGIPATMPDGQGQTSNIDLSSVQNVEVLRGPFSALYGNAS--G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 VGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAG--
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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15-JUN-2002 (Rel. 41, Last anno
Vitamin Bl2 receptor precursor.
BTUB OR SYR4130.
Salmonella typhimurium.
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P37409;
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PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Cobalt transport; Transpor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M89481; AAA27031.1; -. EMBL; AE008893; AAL22968.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=LT2 / SGSC1412 / ATCC 70072
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93079446; PubMed=1448622;
Wei B.Y., Bradbeer C., Kadner R.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.":
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                           RHETFYAAAD-----WDINPDTVLGAGYLYQQRHLAPYN-GLPADANNKLPSLPQHVFV
                                                                                                                                    NIDGLPAQMQSINGTLPNLFAF-----DRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA
                                                                                                                                                                                                                       ATLLTAFSVTAFSAWAQD------TSPDTLV-----
                                                                                                                                                                                                                                                 ATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microbiol. 143:459-466(1992)
 LSKTLYGALEHTFSDRWS---GFVRGYGYDNRTDYDAYYSPGSPLIDTRKLYS--
                                                      TELTAGWGSNSYQNYDISTQQQLGENTRATLIGDYEYTKGFDVVAKGGTGMQAQPDRDGF
                                                                                FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGR--
                                                                                                            LIDGVRLNLAGVSGS-ADLSQFPVSLVQRIEYIRGPRSAIYGSDAIGGVVNIITTRDNPG
                                                                                                                                                                RSAVLAPVTIVTRODIERWQSTSVNDVLRRLPGVDIAQSGGAGQNSSIFIRGTNSSHVLV
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                                                                                                                                                                                                                                                                                            Similarity
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614 AA;
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21.1%;
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Pred.
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> P (IN REF. 1).
> I (IN REF. 1).
> S (IN REF. 1).
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C-TERMINAL
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No. 1.3e-06;
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QSWDA
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van Hove B
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SEQUENCE
                        of iron dicitrate transport in Esc
J. Bacteriol. 172:6749-6758(1990).
                                                                                                                                                                    MEDLINE=95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, So
                                                                                                                                                                                                STRAIN=K12 / N
                                                                                                                                                                                                                                        J. Bacteriol.
                                                                                                                                                                                                                                                              Pressler U., Staudenmaier H., Zimmermann L., Brau "Genetics of the iron dicitrate transport system
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
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01-FEB-1995 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P13036;
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                                     "Novel two-component transmembrane transcription control: of iron dicitrate transport in Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                              Escherichia
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                                                                                         SEQUENCE OF 1-428 FROM
                                                                                                                                                                                                                                                                                          MEDLINE=88227855;
                                                                                                                                                                                                                                                                                                                                                                                                      FECA OR B4291
                                                                                                                  Analysis of the Escherichia coli genome region from 92.8 through 100 minutes."; ucleic Acids Res. 23:2105-2119(1995).
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                                                                                                                                                                                                 / MG1655;
731-774 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        coli
                                                               2220; PubMed=2254251;
Staudenmaier H., Bra
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                                                                                                                                                                                                                                       170:2716-2724 (1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                               Braun V.;
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                                                                                                                                                                      Sofia H.J.,
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Pfam; PF00593; TonB boxC; 1.
PROSTIE; PS00430; TONB DEPENDENT REC 1; 1.
PROSTIE; PS01156; TONB DEPENDENT REC 2; 1.
Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor; Complete proteome.
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                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Outer membrane.
-!- INDUCTION: FOR INDUCTION THE TONB AND THE EXBB PROTEIN HAVE TO ACTIVE. REGULATION BY THE INON LEVEL MEDIATED BY THE FUR PROTEIN AND INDUCTION BY CITRATE PLUS IRON SUGGEST THAT THE IRON(III) DICTIRATE COMPLEX MUST ENTER THE PERIPLASM WHERE IT BINDS TO A TRANSMEMBRANE PROTEIN, MICH REGULATES DIRECTLY OR VIA A FURTHER INDUCTOR, TRANSCRIPTION OF THE FEC GENES.
-!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
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                                                                                         transport
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                                        Staudenmaier H., van Hove B., Yaraghi Z., Braun V.;
"Nucleotide sequences of the fecBCDE genes and locations of the proteins suggest a periplasmic-binding-protein-dependent transpormechanism for iron(III) dicitrate in Escherichia coli.";
J. Bacteriol. 171:2626-2633 (1989).
-!- FUNCTION: FECA IS THE OUTER MEMBRANE RECEPTOR PROTEIN IN THE IRON(III) DICITRATE TRANSPORT SYSTEM.
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T -> M (IN REF. 1 AND 3).
W -> R (IN REF. 1).
L -> V (IN REF. 1).
L -> V (IN REF. 1).
K -> A (IN REF. 1).
W; 16BSBS10276C3B09 CRC64;
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Pred. No. 1.8e-06;
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                          MEDLINE=89213950; PubMed=2651410;
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EMBL, M63115; AAA23768.1; -...
EMBL, M26397; AAA23761.1; -...
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EcoGene; EG10286; fecA.
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Stojiljkovic I.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN IS INVOLVED IN THE INITIAL SIEP OF IRON
UPTAKE BY BINDING HEMIN, AN IRON CHELATIN SIDEROPHORE THAT ALLOWS
THE BACTERIA TO EXTRACT IRON FROM THE ENVIRONMENT.
                                                                                                                                                                                                                                                                                                                             284 GGTADNGFGTALLYSGTRGSDWREHSATRIDDLMLKSKYAPDEVHTFNSLLOYYDGEADM 343
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ONNPKETHNLMV 283
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SECOLISTANDANCE 51872 / WA-C / Serotype O:8;
MEDLINE-93049186; PubMed=1425573;
Stojiljkovic I., Hantke K.;
"Hemin uptake system of Yersinia enterocolitica: similarities with "Hemin uptake systems in Gram-negative bacteria.";
EMBO J. 11:4359-4367(1992).
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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SIGNAL
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PIR; S28042; S28042; TonB_boxC.

InterPro; IPR000531; TonB_boxC.

Pfam; PF00593; TonB_boxC; 1.

PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.

PROSITE; PS01156; TONB_DEPENDENT_REC_2; FALSE_NEG.

Outer membrane; Iron transport; Transport; TonB_box; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y--NIDGLPAQMQS--INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIV-----NL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
                             VSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEG------VETEISGAVTPKW
                                                                                        VYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMD-----DRLNAR
                                                                                                                                                                                      FPOADI-REGSGWLQDEITL----
                                                                                                                                                                                                                  VIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANAR-KGVRGYSHTVATENL 444
                                                                                                                                                                                                                                                                                                                                               FVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMK-----
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                                                                                                                         DKWSSRGAVSVTPTDWLMLFG--------SYAQAFRAPTMGE
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                                                                                                                                                                                                                                                                                  -TPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNT------ANEF 385
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687 AA;
                                                           NDSKHFSMNIMGNTLTNYWVPNPNLKPETNETQEYGFGLRFNDLMMAEDDLQFK
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687 H
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75226 MW;
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-KDYISTGVTMDFGFGPGGLYCKNCSTYSTNIDRAKIWGW
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Pred. No. 3.3e-06;
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TONB BOX.
TONB C-TERMINAL
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Matches 174; Conserv
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SEQUENCE
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SIGNAL
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Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: RECEPTOR FOR CLOACIN DF13/AEROBACTIN.
-i- SUBCELLULAR LOCATION: Outer membrane.
-i- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krone W.J.A., Stegehuis F., Koningstein G., van Doorn C., Roosendaal B., de Graaf F.K., Oudega B.; "Characterization of the pColV-K30 encoded cloacin DF13/aerobactin outer membrane receptor protein of Escherichia coli; isolation and purification of the protein and analysis of its nucleotide sequence and primary structure."; FEMS Microbiol. Lett. 26:153-161(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IUTA_EC
P14542;
                                                                                                                                                                                                                                     InterPro; IPR000531; TonB_boxC.
Pfam; PF00553; TonB boxC; 1.
PROSITE; P800430; TONB DEPENDENT_REC_1; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Iron transport; Transport;
                                                                                                                                                                                                                                                                                                                    EMBL; X05874; CAA29297.1;
EMBL; X05874; CAA29298.1;
PIR; S01042; S01042.
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01-NOV-1995 (Rel.
15-JUL-1999 (Rel.
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Bacteria; Proteobacteria;
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                                                            SVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTK
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32, Last sequence update)
38, Last annotation updat
receptor precursor (Cloac
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                                                                                                      Score 198;
Pred. No.
                                                                                                                                                                 FERRIC AEROBACTIN RECEPTOR TONB BOX.
TONB C-TERMINAL BOX.
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                                                                                          Mismatches
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(Cloacin
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                                                                                                                                                     -----QYKAEADV--SGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAA 240
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                                                                  100 VVL-VDGVRLNSSRTDSRQLDSIDP----FNMHHIEVIFGATSLY-GGGSTGGLINIVT 152
                                         SEYNIDGL------PAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR 174
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                                                                                                                          153 KKGOPETMMEFEAGTKSGFSSSKDHDERIAGAVSGGNEHISGRLSVAYOKFGGWFDGNGD
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                                                                                                                                                                                                                                                               296 HDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGR----
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                KR----PTKAFQGHAAAGFGTHK--------
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STRAIN-KIM6;
MEDLINE-96386041; PubMed-9026634;
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HMUR OR YPO0283.
Yersinia pestis.
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EMBL; AJ414141. CAC89146.1; -.

InterPro; IPR000531; TOAB\_boxC.

Pfan; PF00593; TOAB\_boxC.

PROSITE; PS00410; TOMB\_DEPENDENT\_REC\_1; 1.

PROSITE; PS01156; TOMB\_DEPENDENT\_REC\_2; FALSE\_NEG.

Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor; MEDLINE=21470413; PubMed=11586360; ParkIN=21470413; PubMed=11586360; ParkIN11 J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebainla M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelron J., Stevens K., Whitehead S., Barrell B.G., "Genome sequence of Yersinia pestis, the causative agent of plague."; Nature 413:523-527(2001).

-i- FUNCTION: THIS PROTEIN IS INVOLVED IN THE INITIAL STEP OF IRON UPTAKE BY BINDING HEMIN, AN IRON CHELATIN SIDEROPHORE THAT ALLOWS THE BACTERIA TO EXTRACT THOON FROM THE ENVIRONMENT.

-i- SUBCELLULAR LOCATION: Outer membrane.

-i- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS. SVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSS---VYARGYEYSEY--NIDGL 130 MYTVIEGNAPTSQTAATAADMLKQVPGLTVTGS--GRTNGQDVVMRGYGKQGVLTLVDGV 120 131 PAQMQS--INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIV------NLVRKRPTKA 180 181 FQGHAAAGFGTH-----KQYKAEADVSGSLN----SDGSVRGRVMAQTVGASPRPAEKN 230 231 NRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNK 290 ETISNVLAKGTWOIDSIQSLSANLRY-----YNNSAIEPKNPOTSAPSSTNVMTNRST 285 FKWNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMK-----TPAGRPG 344 Query Match 5.2%; Score 195; DB 1; Length 676; Best Local Similarity 19.1%; Pred. No. 7.2e-06; Matches 147; Conservative 104; Mismatches 306; Indels 214; Gaps LAALSSSVFAAQTADLETVHIKGQR--SYNAIVTEKNGDYSSFAVTVGTKIPASLREIPQ 75 16 LAIACTLPLATQAADTTTTQTSSKKHSTDTMVVTATGNERSSF------EAPM 62 YRVYSSAATGDHSFGLGASAFGRTDDLDGILSFGTRDIGNIR----QSNGFN--APND φ Hornung J.M., Jones H.A., Perry R.D.;
"The hmu locus of Yersinia pestis is essential for utilization free haemin and haem-protein complexes as iron sources.";
MOI. Microbiol. 20:725-739(1996). 84ED731CB914ACD3 CRC64; HEMIN RECEPTOR.
TONB BOX.
TONB C-TERMINAL BOX. or send an email to license@isb-sib.ch). POTENTIAL 74230 MW; 28 676 51 676 659 ( 676 AA; SEQUENCE SIGNAL 18 9/ 63 181 291 合 q g ò ò g ò ò ò 8 ò 셤

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01-NOV-1988 (Rel. 09, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
MEDLINE=97061202; PubMed=8905232; Oshima T., Aiba H., Baba T., Fuji Ikemoto K., Inada T., Itoh T., Ka
                                                                              SEQUENCE F
                                                                                                                                                  SEQUENCE FROM N.A.

Chung E., Allen E., Araujo R., Aparicio A., Davis Federspiel N., Hyman R., Kalman S., Komp C., Kurdi Lin D., Namath A., Oefner P., Roberts D., Schramm Submitted (JAN-1997) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                         Science
                                                                                                                                                                                                                                                                                                                                                                        Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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"Nucleotide sequence of the gene for the
"T--harinhia coli. Homology among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=86278160; PubMed=3015941;
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1ce 277:1453-1474(1997).
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                            Fujita K.,
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  Kajihara
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Hayashi K., H
M., Kanai K.,
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Lew H.
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Sampei G., Sent
Horiuchi 7
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PDB; IFEP; 13.JAN-99.
ECO2DBASE; D079.0; 6TH E
ECOGene; EG10293; fepA.
InterPro; IPR000531; Ton
Pfam; PF00593; TonB_boxC
                                                                CONFLICT
CONFLICT
SEQUENCE
                                                                                                             SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchanan S.K., Smith B.S., Venkatramani L., Xia D., Esser L., palnitkar M., Chakraborty R., van der Helm D., Deisenhofer J.; Palnitkar M., Chakraborty R., van der Helm D., Deisenhofer J.; "Crystal structure of the outer membrane active transporter FepA Escherichia coli.; Nat. Struct. Biol. 6:56-63 (1999).

-i- FUNCTION: THIS PROTEIN IS INVOLVED IN THE INITIAL STEP OF IRC UPTAKE BY BINDING FERRIENTEROBACTIN (FE-ENT), AN IRON CHELATI UPTAKE BY BINDING FERRIENTEROBACTIN (FE-ENT), AN IRON CHELATI SIDERELULULAR LOCATIONS E. COLI TO EXTRACT IRON FROM THE ENVIRONMENT. FEPA ALSO ACTS AS A RECEPTOR FOR COLICINS B AND -1- SUBCELULULAR LOCATION: Integral membrane protein. Outer membra-1- SIDECELULULAR LOCATION: Integral membrane protein. Outer membra-1- SIDECELULULAR LOCATION:
                                                                                                                                                                                                                                                                                                                             EMBL; M13748; AAA65994.1; -.
EMBL; AE000163; AAC73685.1; -.
EMBL; U82598; AAB40783.1; ALT_INIT.
EMBL; D90700; BAA35225.1; -.
EMBL; J04216; AAA23756.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Transcriptional mapping and nucleotide sequence (coli fepA-fes enterobactin region. Identification iron-regulated bidirectional promoter.";
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Mori H., Motomura K., Nakamura
Sampei G., Seki Y., Tagami H.,
                                                                                                                                                            Signal; Receptor; 3D-structure; Complete SIGNAL 1 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaborabetween the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                     PROSITE; PS00430; TŌNB_DEPENDENT_REC_1; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Transmembrane; Outer membrane; Iron transport; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90354449; PubMed=2201687;
Armstrong S.K., Francis C.L., McIntosh
"Molecular analysis of the Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                iron-regulated
J. Biol. Chem.
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                    Similarity
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Pred. No. 1.1e
8; Mismatches
                   Score 193.5; DB 1;
Pred. No. 1.1e-05;
                                                                A -> R (IN REF. 1).
MISSING (IN REF. 1).
; 09348AAB1C29710A CRC64;
                                                                                                             TONB BOX.
TONB C-TERMINAL BOX.
                                                                                                                                            FERRIENTEROBACTIN RECEPTOR.
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a Y., Nashimoto H
, Takemoto K., Wa
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VSIITNQQVKDRNV-DTFDQLARKTPGLRVLSN-----DDGRSSVYARGYEYSEYNID

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LNEFRSIPQVDLIANARKGVRGYSHTVAT -- ENLDEFGIYGKSTFHPADGLSLIGGGRLG 470
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                                           GLPAQMQS------INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLV 173
                                                                                                        174 RKRPTKAFQGHAAAGFGT--HKQ----YKAEADVSGSLNSDGSVRGRVMAQTVGASPRPA 227
                                                                                                                                                                     EKNNRHETFYAAAD------WDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQH 281
                                                                                                                                                                                                                                  VFVGAD-----WNKFKMNSHDVFADLKHYFGNGGYGKVGMRYS-DRDADSNYAFAGSKL 334
                                                                                                                                                                                                                                                                                              ---PAGRPGCNTA--DDKACAVG 356
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                                                                                                                                                                                                                                                                                                                                                         LGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFR----STNEQGRTTLYARGGLA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----QINLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNK 571
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                                                                                                                                                                                                  -----LYGNLDKTQADAWDIN-------QGHQSARAGTYA---TTLPAGREG
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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Rhizobium meliloti (Sinorhizobium meliloti)
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or send an email to license@isb-sib.ch).
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EMBL; AB007312; AAK65923.1; -.
InterPro; IPR000531; TONB_boxC.
Pfam; PF00593; TONB_DDXC; I.P.
PROSITE; PS00400; TONB_DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; FALSE_NEG.
Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor; Plasmid; Complete proteome.
                                                                                                                                                    biosynthesis,
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268 KQDSDYGLYYGPFFAALADPSLFETRSGYESDFNPQTRRSMLNVTYTDNDVFGQQLLLQG 327
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MEDLINE=21172875; PubMed=11274118;
Lynch D., O'Brien J., Welch T., Clarke P., Cuiv P.O., Crosa J.H.
O'Connell M.;
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larity 18.9%; Pred. No. 1.1e-05;
Conservative 116; Mismatches 308; Indels 277.
                                                                                                                                              "Genetic organization of the region encoding regulation, bio and transport of rhizobactin 1021, a siderophore produced by Sinorhizobium melloti."

J. Bacteriol. 183:2576-2585(2001).
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16AE44A4025D5B23 CRC64;
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"Nucleotide sequence of the gene for
in the outer membrane of Escherichia
                                                                       SEQUENCE OF 1-5 FI
MEDLINE=91154132;
                                                                                                                                         "Analysis of the Escherichia coli genome. region from 89.2 to 92.8 minutes."; Nucleic Acids Res. 21:5408-5417(1993).
                                                                                                                                                                                                                                 STRAIN=K12 / MG1655;
MEDLINE=94089392; PubMed=8265357;
Blattner F.R., Burland V.D., Plun
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CT-1993 (Rel. 27, Last sequence up
CT-2001 (Rel. 40, Last annotation
min B12 receptor precursor.
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                                            C., Lindstroem P.H.,
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regulatory
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                                              Hagervall T.G.,
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Best Local
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CONFLICT
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SEQUENCE
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EMBL; U00006; AAC43072.1; -.
EMBL; AS000471; AAC76948.1; -.
EMBL; M57568; -; NOT ANNOTATED CDS.
EMBL; L14556; AAA23676.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Point mutations in a conserved region (TonB box) of Escherichia outer membrane protein BtuB affect vitamin B12 transport.";
J. Bacteriol. 171:6526-6533(1989).
-i- FUNCTION: COBALAMIN RECEPTOR PROTEIN. ALSO ACTS AS A RECEPTOR BACTERIOPHAGE BF23 AND IS NECESSARY FOR THE UPTAKE OF E COLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93106943; PubMed=8093236;
Dougherty T.J., Thanassi J.A., Pucci M.J.;
"The Bscherichia coli mutant requiring D-glutamic
of mutations in two distinct genetic loci.";
J. Bacteriol. 175:111-116(1993).
                                                                                                                                                                                                                                                                                    Phage
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                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                              PROSITE; PS00430; TONB DEPENDENT REC 1; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Cobalt transport; Transpor
                                                                                                                                                                                                                                                                                                                                           EcoGene; EG10126; btuB.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGENESIS OF TONB BOX.
MEDLINE=90078094; PubMed=2687240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cink A.J., Robison K., Church G.M.;
"Comparing the predicted and observed projin the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  common with the rRWA P1 promoter family of Escherichia coli.", J. Bacteriol. 173:1757-1764 (1991).

    -!- SUBCELLULAR LOCATION: Outer membrane.
    -!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kadner R.J.
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RSTVLAPTTVVTRQDIDRWQSTSVNDVLRRLPGVDITQNGGSGQLSSIFIRGTNASHVLV
                         QS-----VSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDG--RSSVYARGYEYSE--Y 125
                                                    ASLLTACSVTAFSAWAQD
                                                                              ATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIP
                                                                                                                                                                                                                                                                                      recognition; Receptor;
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V->G: INACTIVATE UPTAKE.
A -> G (IN REF. 1).
A -> R (IN REF. 1).
A -> R (IN REF. 1).
                                                                                                                      Score 191;
Pred. No. 1
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L->P: INACTIVATE UPTAKE
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                                                    -TSPDTLV
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                                                                                                                      DB 1;
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NIDGLPAQMQSINGTLPNLFAF----DRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA 180
                      --OSWD----- 29THSYSHSKDYNY--- 297
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-!- FUNCTION: RECEPTOR FOR THE HYDROXAMATE SIDEROPHORE, FERRICHROME.
BINDS ALSO TO MOST OTHER FERRICHROME DERIVATIVES EXCEPT ENANTIO
FERRICHROME AND FERRIC RHODOTORULATE.
-!- SUBCELLULAR LOCATION: OUTER MEMBYTANE.
-!- INDUCTION: BY IRON STARVATION. IRON REGULATION MEDIATED THROUGH
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(Rel. 32, Last sequence update)
(Rel. 33, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIPEPPSSTLNYGQSW------VYTDMETTF-----GMLRSEYDVSQNWTVYGS 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KLGMKTPAGRPGC----NTAD-----DKACAVG-----LGTEIKQKALA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 VGASRNEETGQYGAPMLTNNNGDATISRLYVPYVADSVAGLGGIRGHFDTGPITHKVNLG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YAANYRTIKSAWNMSGQEDINIYNPGVIGFPQTVMGSDSQDPQLTSQVRASGLSLSDTLS 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  466 GGRLGHYKIES-GEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADG 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-----HIEALGPGKS-----GPYQYNGK------PVVNA---G 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLLKPROGNOPEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTR-YAALGKRVM 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQVTPEL 643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAALSSSVPAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTK-----IP
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                                                                                                                                                                                                                                                         PROSITE; PS00430; TÖNB DEPENDENT REC 1; 1.
PROSITE; PS01156; TONB DEPENDENT REC 2; 1.
Signal; Receptor; Transmembrane; Outer membrane; Iron transport;
               SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                               5.0%; Score 190.5; DB 1; Length 758; 19.8%; Pred. No. 1.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IndelB
                                                                                                                                                                                                                                                                                                                                                                                                            81749 MW; 945675B0DEF49F7C CRC64;
                                                                                                                                                                                                                                                                                                                                                      FERRICHROME RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 103; Mismatches 354;
                                                                                                                                                                                                                                                                                                                                                                     TONB BOX.
TONB C-TERMINAL BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .7e-05
                                                                                                                                                                                                     EMBL, X67331; CAA47746.1; -.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
                                                                                                                                                                                                                                                                                                                   TonB box.
                                                                                                                                                                                                                                                                                                                                                                                                            758 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Sim
Matches 162;
                                                                                                                                                                                                                                                                                                                     Transport;
SIGNAL
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                                                                                                                            Matches
                                                                                                                                                   Query Match
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01-OCT-1993
01-OCT-1993
                                                                                                                                                                                                                                                        PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEIGO
                                                                                                                                                                                                                  SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outest the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/amor send an email to license@isb-sib.ch).
                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                              EMBL; M96731; AAA25503.1; -.
PIR; A43335; A43335.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cornelissen C.N., Biswas G.D., Tsai J., Paruchu: Thompson S.A., Sparling P.F.; "Gonococcal transferrin-binding protein 1 is reutilization and is homologous to TonB-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferrin-binding protein 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92394880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptors."
 118
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                          58
                                                  58
                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol. 174:5788-5797(1992).
- FUNCTION: ACTS AS A TRANSFERRIN RECEPTOR AND IS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSFERRIN UTILIZATION. SUBCELLULAR LOCATION: Ou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEIGO
                                                                                                QFMSVFRIN---MTAATVLAALSSSVFA--AQTADLETVHIKGQRSYNAIVTEKNGDYSS
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                                                                        QQQHLFRLNILCLSLMTALPAYAENVQAGQAQEKQLDTIQVKAKKQKTRRDNEVTG----
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-RGYEYSEYN--IDGLPAQMQS---
                                               FAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA 117
                                                                                                                                                                                                                                             membrane;
                                                                                                                                       Similarity
                                                                                                                                                                                                                                        PS00430; TÖNB_DEPENDENT_REC_1;
PS01156; TONB_DEPENDENT_REC_2;
mbrane; Receptor; Signal; TonB t
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898
915 /
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(Rel. 27, Last sequence update)
(Rel. 32, Last annotation updat
                                                                                                                            Conservative
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                         LGKLVKTADTLSKEQVLD-----IRDLTRYDPGIAVVEQGRGASSGYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=1325963;
                                                                                                                                                                                         915
45
915
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                                                                                                                                                                            102213 MW; 697CF74B1010422F
                                                                                                                          100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Outer membrane
                                                                                                                                                                                        TRANSFERRIN-BINDING TONB BOX.
TONB C-TERMINAL BOX.
                                                                                                                                       Score 172;
Pred. No. 0.
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 --INGTLP----
                                                                                                                           Mismatches
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-NLFAFDR---VEVMRGPSG
                                                                                                                                                 Length 915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            outer membrane
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FQ
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RESULT 30
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SEQUENCE OF 25-45
STRAIN=CCUG 37603
MEDLINE=93307625;
                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE STRAIN=CCUG 37603 / B1686 / Seroc MEDLINE=93345825; PubMed=8344530
                                                                                                                                                                                                                                     01-FEB-1995
16-OCT-2001
                                                                 encoding
                                                                                                                                                                                  Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision;
                                                                                                                                                                                                                                                              01-FEB-1995
                                                                                                                                                                    NCBI_TaxID=491;
                                                                                                                                                                                                             TBP1.
                                                                                                                                                                                                                                                                           Q06987;
                                                     Gene 130:73-80(1993).
                                                                                                                                                                                                                        Transferrin-binding protein 1 precursor
                                                                            Cloning
                                                                                        acobs E.,
                                                                                                   egrain M., Mazarin V.,
                                                                                                                                                                                                                                                                                                                                                          655
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                                                               and characterization of
the transferrin-binding
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                                                                                         Schryvers A.B.;
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(Rel. 31, Last sequence update)
(Rel. 40, Last annotation updat
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 / B16B6 / Serogroup
PubMed=8319886;
                                                                                                                              AND SEQUENCE OF 25-42.
B16B6 / Serogroup B /
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                                                                                                    Irwin S.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QQQHLFRLNILCLSLMTAL--PVYAENVQAEQAQEKQLDTIQVKAKKQKTRRDNEVTG-- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Griffiths E., Stevenson P., Byfield P., Ala'Aldeen D.A., Borriello S.P., Holland J., Parsons T., Williams P., "Antigenic relationships of transferrin-binding proteins from Neisseria meningitidis, N. gonorrhoeae and Haemophilus influenzae: cross-reactivity of antibodies to NH2-terminal peptides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 QFMSVFRINMTAATVLAALSSSVFA-----AQTADLETVHIKGQRSYNAIVTEKNGDY
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                                                                FEMS Microbiol. Lett. 109:85-91(1993)

-!- FUNCTION: ACTS AS A TRANSFERRIN RECEPTOR AND IS REQUIRED FOR TRANSFERRIN UTILIZATION.

-!- SUBCELLULAR LOCATION: Outer membrane.

-!- INDUCTION: BY IRON STRANVATION.

-!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 125; Mismatches 330; Indels 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 908;
                                                                                                                                                                                                                                                                                                                                                                                     TRANSFERRIN-BINDING PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                   45 TONB BOX.
908 TONB C-TERMINAL BOX.
101583 MW; FE2FF4974CAC3C31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.4%; Score 167.5; DB 1
18.2%; Pred. No. 0.00085;
                                                                                                                                                                                                                                                                                                      Interpro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PR051TE; PS00430; TONB_DEPENDENT_REC_1; 1.
PR051TE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Receptor; Signal; TonB_box.
                                                                                                                                                                                                                                                                EMBL; Z15129; CAA78831.1; -. PIR; JN0819; UN0819. PIR; S33154; S33154.
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891 9
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    655 GESLKTLDLKPEKSFNREAGIVFKGDFGNLEASYFNNAYRDLIAFGYETRTQNGQTSASG 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       715 DPGYRNAQNARIAGINILGKIDWHGV------WGGLPDGLYSTLAYNRIKVKDA- 762
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377 RLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANAR----KGV
                                                   DTAKIRHNLSINLGYDRFKS--QLSHSDYYLQ-----NAVQAYDLITPKKPPFPNGS
                                                                                                                                                                                                                                                KDNPYRVSIGKTTVNTSPICRFGNNTYTDCTPRNIGGNGYYAAVQDNVRLGRW-ADVGAG
                                                                                                                                                                                                                                                                                                                                 ----KTLHKASKTKFTG-----YAGAV-----YDLNDNNSLYL---SLSQLYTPQT
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-!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
-!- SIMILARITY: LOW, TO THE CORRESPONDING PROTEIN IN SEROTYPE D
HINPLUENZAE.
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Haemophilus
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"A gene cluster involved in the utilization of both free hy
meen-themopexin by Haemophilus influenzae type b.";
J. Bacteriol. 177:264-2653(1995).
-i- FUNCTION: REQUIRED FOR UTILIZATION OF FREE HEME AT LOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
10-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Heme/hemopexin utilization protein C precursor
                                                                                                                                                                   RGYSHTVA----TENLDEFGIYGKSTFHPADGLSLIGGG--
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InterPro, IPR000531; TonB_boxC.
Pfam, PF00593; TonB_boxC, 1.
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STRAIN=DL42 / Serotype B;
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RESULT 32
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Best Local S
Matches 167
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PROSITE; PS01156
Outer membrane;
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les 167; Conser
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                                                                                                           LKGEWKNLRLDFALENLFDRKYQP----AFSLMEGTGRNAKISAVYSF
                                                                                                                                                                                                                                                                                          TANLHFDSLF---KOGDKFKIEATYFRNDVKDFINLKIFNDAKTNTNASASAGAGAGANP
                                                                                                                                                                                                                                                                                                                                                      IVTNWLDFTAKYNEAFRAPSMQERFVSGSHFGTSILGRNEINKFVANPNLRPETAKNKEI
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                                                                                                                                                                    SNIAASKIGVGVNYALVKDKFTVGATVTHYAAQRRVPKDHSVTYPSYILTDLRATY--AP
                                                                                                                                                                                                L-MPKHSANLWTTYQ-VTPELTIGGGVN---AMSGITSSAGMHAGGYATFDAMAAYRFTP
                                                                                                                                                                                                                                                                                                                        --NLDADGKLLKPRQGNQF--EVGYKGSYMDDRLNARVSFYRMKDKNAAAP-----LNP
                                                                                                                                                                                                                                                                                                                                                                                 -----FTGYAGAVYDLNDNNSLYLSLSQLYT----
                                                                                                                                                                                                                                                                                                                                                                                                                TTGVYLIAHIPLFGEK-----LLLSPSVRYDHYDTSS---KTVKYKDNHLSPATKLTW
                                                                                                                                                                                                                                                                                                                                                                                                                                              TVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTL-----HKASKTK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SELSHISFVYGVDYMRDKIRTERGTNNKDA-----QFRADPY-----NAN----SN
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                                                                                                                                      -----KLKLQINADNI FNRHYYARVGGANTFNI - PGSERTWTANLRYSF
                                                                                                                                                                                                                            NGALLPTKSQYQNITNARLSGIELQ-AQYQTERLTLFTNYG-----STKGKDKDSGEAL
                                                                                                                                                                                                                                                            NN----KKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFL
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PS01156; TONB_DEPENDENT_REC_2; 1.

mbrane; Transport; TonB box; Signal; Receptor.

1 19 OR 21 (POTENTIAL).

20 725 HEME/HEMOPEXIN UTILIZATION PROTEIN
725 AA; 80838 MW; FC7886E020CB5BCE CRC64;
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                                 STANDARD;
   40, Created)
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Best Local Sim:
Matches 168;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemoglobin-haptoglobin utilization protein B
HPUB OR NMA0474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SIGNAL 1
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PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Transport; TonB box; Signal; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL162753; CAB83769.1; -.
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-!- FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN OR HEMOGLOBIN/HAPTOGLOBIN COMPLEX AND IS REQUIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Z2491 / Serogroup A / Serotype 4A;
MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
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SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY)
                          SLPQHVFVGADWNKFKMNSHDVF-----ADLKHYFGNGGYGKVGMRYSDR------
                                                                                  GPSKYLTYVATGVARSQPDPQEW-VNKSTLFKLGYNFNDQNRIGWIFEDSRTDRFTNELS
                                                                                                                                    KNNRHETFYAAA-----DWDINPDTVLGAGYLYQQRHLAPY---NGLPADANNKLP
                                                                                                                                                                                              ITAAGRLFGLDALLVYTRRFGKETKNRSTEGDI--EIKNDGYV-
                                                                                                                                                                                                                                                         HAAAG----
                                                                                                                                                                                                                                                                                                           NFSEVTITKGADSLKSGSGALGGAVNYQTKSASDYVSEDKPYHLGIKGGSVGKNSQKFSS 196
                                                                                                                                                                                                                                                                                                                                                                                                                       VEGGRAGSNGFTIRGVDKDRVAINVDGL-AQAESRSSEAFQELFGAYGNFNANRNTSEPE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSNDDGRSSVYA-RGYEYSE--YNIDGLPAQ-----MQSINGTLPNLFA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPAFAADPAPQSAQTLNEITVTGTHKTQKLGEEKIRRKTLDKLLVNDEHDLVRYDPGISV
                                                                                                                                                                                                                                                                                                                                                                  -FDRVEVMRGPSGLFDSSGEMGGIVNLVRK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   810 AA;
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810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 162.5; DB pred. No. 0.0016;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation enter EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                  610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    667 GK-ATQNNGKETPINALSP-----WTAV-----YSLGYDAPSKRWGINAYATRTAAKKP 714
                                          DADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKOKALAFD----ASYSRPF 376
                                                                                 DIPKNYDKRGINGEVYHSFRHIRONTAQ-----WTADFEKQLDFSKAVWAAQYGLGG 414
                                                                                                                                                                                                       HTVATENLDEFGI-YGKSTFHPADGLSLIGGGRLGHYKIESG---------477
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-TMLIENRSKYKFAYWNNAFH-----LGGN--DRFRLNAGIRYDKNSSSAKDDPKYTT 493
                                                                                                                                                                                                                                                                                                                                                                           519 NLDADGKLLKPRQGNQFEVGYKGS----------YM----DDRLNARV 552
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NLWTGTTTSAATGDYR-HRQDVSYRRRSGVEYKNELEHGPWDSLKLRYDKQRIDMNTWTW 362
                                                                                                                                                                                                                                                                                                                                 494 AIRGQIPHLGSERAHAĞFSYCTGFDWRFTKHLHL-LAKYSTGFRAPTSDETWLLFPHPDF 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               715 SDTVHSNDDLNNPWPYAKHSKAYTLFDLSAYLNIGKQVTLRAAAYNITNKQYYTWESLRS 774
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                                            377 RLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYS
                                                                                                                                                                                                                                                                                        --EGKTLHKASKTKFTGYA-GAVYDLNDNNSLYLSLSQLYT------PQT
                                                                                                                                                                                                                                                                                                                                                                                                                  553 YLKANPN-LKAEKAKNWÉLGLAGSGKAGNFKLSGFKTKYRDPIELTYMGVSSDDKNNPR-
                                                                                                                                                                  GKGDNAN----SDYSYF----AKLYDPKILASNQAKI-----SDYSYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Legrain M., Mazarin V., Irwin S.W., Bouchon B., Quentin-Millet M. Jacobs E., Schryvers A.B.;
"Cloning and characterization of Neisseria meningitidis genes encoding the transferrin-binding proteins Tbp1 and Tbp2.";
Gene 130:73-80(1993).
-!- FUNCTION: ACTS AS A TRANSFERRIN RECEPTOR AND IS REQUIRED FOR TRANSFERRIN UTILIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBCELLULAR LOCATION: Outer membrane.
-i- INDUCTION: BY IRON STARVATION.
-i- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=CCUG 37608 / M982 / Serogroup B / Serotype 9;
MEDLINE=93345825; PubMed=8344530;
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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4.3%; Score 161; DB 1; Length 911;
Best Local Similarity 18.3%; Pred. No. 0.0024;
Matches 178; Conservative 133; Mismatches 346; Indels 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSFERRIN-BINDING PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 TONB BOX.
911 TONB C-TERMINAL BOX.
101631 MW; 99283ABAE0B773E6
                                EMBL, Z15130; CAA78833.1; -.
PIR; JN0821; JN0821.
PIR; S33156; S33156.
InterPro; IPR000531; TonB boxC.
Pfam; PF00193; TonB boxC; 1.
PROSITE; PS00430; TONB DEPENDENT REC_1; 1.
PROSITE; PS01156; TONB DEPENDENT REC_2; 1.
Outer membrane; Receptor; Signal; TonB box.
SIGNAL
CHAIN
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911
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     Outer membrane; I
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STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P44600;
01-NOV-1995
01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                 Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B., Gray C., Fountoulakis M.;
"Two-dimensional map of the proteome of Haemophilus influenzae."
Electrophoresis 21:411-429(2000).
-i- FUNCTION: PROBABLE RECEPTOR, TONB-DEPENDENT.
-i- SUBCELLULAR LOCATION: Outer membrane (Potential).
-i- SUMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
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PROSITE; PSO0430; TONB DEPENDENT REC 1; FALSE NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.

Outer membrane; Receptor; Signal; TonB box; Complete |
SIGNAL 1 21 POTENTIAL.
CHAIN 22 723 PROBABLE TONB-DEPENDENT |
SITE 706 723 TONB C-TERMINAL BOX.
                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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Science 269:496-512(1995).
                                                                                                                                         EMBL; U32712; TIGR; HI0262;
                                                                                                                                                                                                                                                                                            This
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                                                                                                        InterPro; IPR000531;
Pfam; PF00593; TonB_
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                                                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collable the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
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(Rel. 32, Last sequence up
(Rel. 41, Last annotation
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                           - PGSERTWTANLRYSF
                                                                                                                                                                                                                                                               QT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQR--SYNAIVTEKNGDYSSFAVTV
MEGTGRNAKISAVYSF
                                                        QRRVPKDHSVTYPSYILTDLRATYAPLKGEWKNLRLDFALENLFDRKYQP-
                                                                                                                QYQTERLTLFTNYGSTKGKDKDSG-EALSNIAASKIGVGVNYALVKDKFTVGATVTHYAA
                                                                                                                                                                                                                                                                                            PATKLTWIVTNWLDFTAKYNBAFRAPSMQERFVSGAHFGANTLGLDHINRFVANPNL-RP
                                                                                                                                                                                                                                                                                                                          SKTKFTG-----
                                                                                                                                                                                                                                                                                                                                                     ----SNTTGVYLIAHIPLFGEK-----LLVSPSVRYDHYDTSS---KTVKYKDNHLS
                                                                                                                                                                                                                                                                                                                                                                                  GVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTL----
                                                                                                                                                                                                                                                                                                                                                                                                               GINLRNSSELSHISFVYGVDYMRDKIRTERGTNGSDAK-----FRADPY----
                                                                                                                                                                                                                                                                                                                                                                                                                                      PFRLGNTAN----EFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DQQIPDQSTVFNYYLTPDNPYLNTHIALYNNKTIEKEQRKVS-GVKDQTKLT-----TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DANNKLPSLPQHVFVGADWNKFKMNSHDV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPNALDLLKNNDKFGVKIROGYQTANNLSEKDVSVFAANDKFDVLISGFYNNADNL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTKIPASLREIPQSVSIITNQQVKDRNVDT---FDQLARKTPGLRVLSND-----DGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRFSKLSLAITTTLVTANA---LAQSVELDSINVIATRDPSRFAYTPEKQSK-DSLLSKQ 56
                                                                                      YRFTPK---
                                                                                                                                             PKHS--ANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGY-----
                                                                                                                                                                                                     NPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLM
                                                                                                                                                                                                                                  ETAKNKEITANLHFDSLF----KQGDKFKIEATYFRNDVKDFINLKI--FNDAKTSASAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSNNEVENELTNEQITDQIKKFHGQKDDLLPPTTQPSPSERSEFYSKVKTRLGSVSY-LT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAQTVGASPRPAEKNNRHETFY-----AAADWDINPDTVLGAGYLYQQRHLAPYNGLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----NLVR----KRPTKAFQGHAAAGFGTHKQY------KAEADVSGSLNSDGSVRGRV 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATSVADALEDIP------NVDVRGGSRSIAQK-PNIRGLSDNRVVQVIDGVR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTGKGNKLNNTAYKQFGGLAKFGWQINDANRV-----ELSHRETRFKQTA
                                                                                                                                                                                                                                                             -NLDADGKLLKPROGNOF--EVGYKGSYMDDRLNARVSFYRMKDKNAAAPL
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19.9%;
                            722
                                                                                                                                                                                                                                                                                                                         -----DNNSLYLSLSQLYTP
                                                                                                                                                                          ---NGALLPK-----NSQYQNITNARLSGIELQA
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L4; Mismatches
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No. 0.0026;
                                                                                     LKLQINADNI FNRHYYARVGGANTFNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301;
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                                                                                                                                              - ATFDAMAA
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                                                                                                                                                                                                                                                                                                                                                                                                               NAN-
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RESULT 35
HPUB\_NEIMC
ID HPUB
AC P9694
DT 16-OC
DT 16-OC

(Rel.

40, Created)
40, Last sequence

update)

HPUB\_NEIMC P96949; 16-OCT-2001

STANDARD;

PRT;

810

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MEDLINE-97251357; PubMed-9097039;
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SEQUENCE OF 464-2003 FROM N.A.
                                                                                                                                                                                                EGVETEISGAVTPKWQ-----
-----VKLYD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corresponding to the 28.
DNA Res. 3:363-377(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=562;
422 SDYSYF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia.
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                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :| :| ; | :| | 257 VARSQPDPQEW-VNKSTLFKLGYNFNDQNRIGWIFEDSRTDRFTNELSNLWTGTTTSAAT 315
                       Neisseria meningitidis (serogroup C).
Bacteria, Proteobacteria, beta subdivision, Neisseriaceae, Neisseria.
NCBI_TaxID=135720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 YSSFAVTVGTKIPASLREI----PQSVSIITNQQVKDRNVDTF-----DQLARKTPGLRV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -FORVEVMRGPSGLFDSSGEMGGIVNLVRKRPT----KAFQ-GHAAAGFGTHKQYKAE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 NFSEVTITKGADSLKSGSGALGGAVNYQTKSASDYVSEDKPYHLGIKGGSVGKNSQKFSS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----NSDGSVRGRVMAQTVGASPRPAEKN--NRHETFYAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----DWDINPDTVLGAGYLYQQRHLAPY---NGLPADANNKLPSLPQHVFVGADW 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 NKFKMNSHDVF-----ADLKHYFGNGGYGKVGMRYSDR------DADSNYAFAGSK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDYR-HRQDVSYRRRSGVEYKNELEHGPWDSLKLRYDKQRIDMNTWTWDIPKNYDLRGIN 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 LGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFD----ASYSRPFRLGNTANEFVIG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATENLDEFG 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 FPAFAADPAPQSAQTLNEITVTGTHKTQKLGEEKIRRKTLDKLLVNDEHDLVRYDPGISV 77
                                                                                                                                                                   utilization operon of Neisseria meningitidis.";
Mol. Microbiol. 23:737-749(1997).
-!- FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN OR THE
HEMOGLOBIN/HAPTOGLOBIN COMPLEX AND IS REQUIRED FOR HEME UPTAKE.
-!- SUBCELLULAR LOCATION: Outer membrane (Potential).
-!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                       the haemoglobin-haptoglobin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 SEVYHSFRHIRONTAQ------WTADFEKQLDFSKAVWAAQYGLGGGRGDNAN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
HEMOGLOBIN-HAPTOGLOBIN UTILIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSNDDGRSSVYA-RGYEYSE--YNIDGLPAQ------MQSINGTLPNLFA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
             B precursor.
                                                                                                                                                                                                                                                                                                                                                                                 EMBL, U73112; AAC44893.2; -.
InterPro; IPR000531; TonB boxC.
Pfam; PR00593; TonB boxC; -1.
PROSITE; PS017 TONB DEPENDENT REC 1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT REC 2; 1.
Outer membrane; Transport; TonB box; Signal; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0D08DD79DA9CB817 CRC64;
                                                                                                                                         D.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       larity 19.1%; Pred. No. 0.0035;
Conservative 109; Mismatches 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TONB C-TERMINAL BOX
                                                                                                                                         Dyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.2%; Score 157.5; DB 1
16-OCT-2001 (Rel. 40, Last annotation update)
Hemoglobin-haptoglobin utilization protein B
                                                                                                             STRAIN=DNM2 / Serogroup C / Serotype 2a;
MEDLINE=97206152; PubMed=9157245;
Lewis L.A., Gray E., Wang Y.-P., Roe B.A.,
"Molecular characterization of hpuAB, the h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90626 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               810 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  793
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Matches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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455 FAYWNNVFH-----LGGN--DRFRLNAGIRYDKNSSSAKDDPKYTTAIRGQIPHLGSE 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Mocomura K., Nakada S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., "A 570-kb DNA sequence of the Escherichia coli K.12 genome
-----PKI-LTSNQAK-----ITMLIENRSKYK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PQTNLDADGKLLKPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----IHAG--YSYLHSQIKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      671 QINGQETPINALSP-----WSAVYNLGYDAPSK---RWGINAYATRTAAKKPSDTVHSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYA------
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland NRIEY M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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STRAIN=Rd / KW20 / ATCC 51907;
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                                                    PS00430; TONB DEPENDENT REC 1; FALSE_NEG.
PS01156; TONB_DEPENDENT_REC_2; 1.
PS01156; TONB_DEPENDENT_REC_2; 1.
PS01156; TONB_DEPENDENT_REC_2; 1.
                                                                                                                                                                                                              non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteobacteria;
 744 AA;
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SEQUENCE FROM N.A., AND SEQUENCE OF 776-796

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                                                                                                                                                                  188 TALVIQNEQKNIDILLFGSVR-----NAGDYKRPDNSKILFSKNNQ-KTGLIKLNWQIS 240
                                                                                                                                                                                                                                                                                                                 ------ADYN-----RFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANA 428
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                                                                               70 ANLINILPGVNMAGGFRPGGQTLNINGMGDAEDVRVQLDGATKSFEKYQQGSIFIEPELL 129
                                                                                                     AFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAG----FGTH-----KQYK 196
                                                                                                                                                                                       PDTVLGAGYLY------QQRHLAPYNGLPADANNKLPSLPQHVFVGAD--WNKFKM 293
 Gaps
                                       ONSSNSNREELLPIIVNTNDD-----SNKLPGR-----SVLKQKNIEQXQADNA 69
                                                                                                                                                                                                                                                                                                                               381 TRNTLMYDKSKVRKADYNYGYFQPYYMPSGRQYTQAFYLQD------QIKWKNIIFST
                    QRSYNA-----IVTEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTF
                                                            DOLARKIPGLRVLSN-DDGRSSVYARGYEYSE---YNIDGLPAQMQSI-NGTL---PNLF
                                                                                                                                               197 AEADVSG-SLNSD----GSVRGRVMAQTVGASPRP-----AEKONRHETFYAAADWDIN
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                                                                                                                                                                                                                                                                                                                                                                                                               294 NSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCN----
                                                                                                                                                                                                                                                                        ---TADD---KACAVG----LGTE--IKQKALAFDASYSRPFRLGNTANEFVIG-----
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Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
269; Indels
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SIITNQQVKDRNVD------TFDQLAKKTPGLRVLS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 EVVEIVGAPPTIDVGSTTMGVNVDQEFIKRIAVARPGGKGGATRSFESLAELAPGAQ--- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDDGRSSVYARGYEYSEYNIDGL----PAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 NDNYGVSINGSTSPENGYVVDGLSTNDPA--FGVNASPLSIEFVQDVNIITG--GYMPEF 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 LONLG------DFGATLGGPILKDKLWFFAGFAPSFTRYOHTRTLNALRVDDE 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 SYNAIVTEKNGDY---------SFAVTVGTKIPASLREIPQSV- 77
                                                                                       Inouye S.;
"Oar, a 115-kilodalton membrane protein required for development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQTVGASPRPAEKNNRHETPYAAADWDINPDTV-LGAGY---LYQQRHLAPYNGLPA-DA
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                                                         Ξ.
                                                                                                                                                                                                      BODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1061;
                                                      Farez-Vidal E., Inouye
                                                                                                                                                                     J. Bacteriol. 175:4756-4763(1993).
-!- FUNCTION: REQUIRED FOR CELLULAR ADHESION DURING FRUITING
                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: OUTER-MEMBRANE ASSOCIATED.
-!- SIMILARITY: LOCAL, TO TONB-DEPENDENT RECEPTOR PROTEINS.
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IW; EA8C077296352EF0 CRC64;
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STRAIN=DZF1;
MEDLINE=93328680; PubMed=8335633;
Martinez-Canamero M., Munoz-Dorado J.,
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1061
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Outer membrane; Signal.
SIGNAL 1 26
                                                                                                                                             Myxococcus xanthus.
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Matches 187; Conserv
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SEQUENCE FROM N.A.

STRAIN-El Tor N16961 / Serotype O1;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamatheyan J., Bass S., Qin H., Dragoi I., Seller

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIUA_VIBCH (
Q00964; Q9JQ00;
01-APR-1993 (Re
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Classical Ogawa 395 / ATCC 39541 / Serotype 01;
MEDLINE=92276356; PubMed=1317381;
Butterton J.R., Stoebner J.A., Payne S.M., Calderwood S.B.;
"Cloning, sequencing, and transcriptional regulation of viuh, gene encoding the ferric vibriobactin receptor of Vibrio chol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25,
01-APR-1993 (Rel. 25,
16-OCT-2001 (Rel. 40,
This SWISS-PROT entry is copyright. between the Swiss Institute of Bio
                                                                                                        "DNA sequence of both chromosomes cholerae.";
                                                                                                                                    Salzberg S.L.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                  STRAIN=Classical Ogawa 395 / ATCC 39541 / Serotype O1; Liao W.J., Choi M.H., Butterton J.R.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio cholerae.
Bacteria; Proteobacteria;
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                                                                                          Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              882
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                                         SUBCELLULAR LOCATION: Outer membrane. SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                          FUNCTION: RECEPTOR FOR FERRIC VIBRIOBACTIN.
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Bioinformatics and the EMBL outstation
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SIGNAL
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Signal; Receptor;
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                                                                              GGRLGHYKIESGE--GKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDAD
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                                                     -ANLGLLKTEFKETTGNTKELPRAPKMSANVGLLYDFG--
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QGFEFSSNAAYTGSYFSESGNS
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TonB_box; Outer membrane; Transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TRAIN=168 / BGSC1A1;

XX MEDLINE=97124196; PubMed=8969509;

XX Voshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,

A wa Y., Fujita Y.;

A miwa Y., Fujita Y.;

Sequencing of a 65 kb region of the Bacillus subtilis genome

containing the lic and cel loci, and creation of a 177 kb contig

covering the gnt-sacXY region.;

Microbiology 142.3113-3123(1996).

I PUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,

MOTILITY, SECRETION OR DIFFERENTIATION.

--- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED

INTO THE MEDIUM.

--- SUBCELLULAR TWO LICAND-BINDING DOWAINS; THE N-TERMINUS, HAS THREE

101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE

C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED

MOTIF REPEATED 31 TIMES.

--- SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME

SIMILARITY TO THE REPEATED MOTIF IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                      | [2]
SEQUENCE FROM N.A.
STRAIN=168 / BGSC1A1;
MEDLINE=95219088; PubMed=7704263;
MEDLINE=95219088; PubMed=7704263;
Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
Yoshida K.-I., Sano H. Seki S., Oda M., Fujimura M., Fujita Y.;
"Cloning and sequencing of a 29 kb region of the Bacillus subtilis
"Cloning and sequencing the "1, 1004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
OR 32 (POTENTIAL),
WALL-ASSOCIATED PROTEIN.
3 X 101 AA APPROXIMATE TANDEM REPEATS.
1-1.
                                                                                                                                                                                                                                                                   "Molecular analysis of three major wall-associated proteins of Bacillus subtilis 168: evidence for processing of the product of gene encoding a 258 kDa precursor two-domain ligand-binding
                                                                                                                     Bacillus subrils.
Bacieria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1423;
                                                (Rel. 30, Created)
(Rel. 30, Last sequence update)
(Rel. 41, Last annotation update)
                   2334 AA
                                                                                                Wall-associated protein precursor.
WAPA OR N17G.
                                                                                                                                                                                                                    STRAIN=168;
MEDLINE-93302506; PubMed=8316082;
                                                                                                                                                                                                                                                                                                                                     Mol. Microbiol. 8:299-310(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CenC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S32920; S32920.
Subtilist; BG10797; wapA.
InterPro; IPR003305; CBM_CenC
Pfam; PF02018; CBM_4 9; I.
Cell wall; Repeat; Signal; Cc
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D83026; BAA11683.1; -. Z99124; CAB15959.1; -.
                   STANDARD;
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869
605
736
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       Foster S.J.;
                                                01-OCT-1994
                                                                   01-OCT-1994
15-JUN-2002
                   BACSU
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EMBL; EMBL;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1712 DPLGNVLASEYDANSNLTKTISPNGNEVSLSYD-----GTDRVKSKSYNGTEKYI 1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1812 KLKTFSWIHGDQKGTNQFTYNKLDQMIEMKDSTSSYSFDYDENGNVQTFITGNGGGTSFS 1871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1666 MTLSNGTSILHSYDKEGNEVSKTIRA------GADOTYKFEYDVMGKLVKTT 1711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --------YGKVGMRYSDRDADSNYAFAGSKLG-MKTPAGRPGCNTA-- 348
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1 X 21 AA APPROXIMATE TANDEM REPEATS OF (4) -G-X(4) - [YF] -X-D-X(2) -G-X(4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVRGRVMAQTVGA-----SPRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VGTKIPASLRE-----IPQS----VSIITNQQVKDRNVDTFDQLARKTP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.6%; Pred. No. 0.4;
tive 93; Mismarches 328; Indels 254; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 INMTAATVLAALSSS-----VFAAQTADLETVH--IKGQRSYNAIVTEKNGDYSSFA-VT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -DDKACAVGL-----GTEIKQKALAFDASYSRPFRLGNTANEFVIGA----DYNRF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 APYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGG------
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16-OCT-2001
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MEDLINE-20316037; PubMed=10858226;

Cope L.D., Hrkal Z., Hansen E.J.;

"Detection of phase variation in expression of "Detection of phase variation in expression of phase variation in expression of "Detection of phase variation in expression of "Detection of phase variation in expression of "Detection of phase variation in expression of "Detection of phase variation in expression of "Detection of phase variation in expression of "Detection of phase variation in expression of "Detection of phase variation in expression of "Detection of phase variation" of phase variation in expression of "Detection of phase variation in expression of "Detection of phase variation" of phase variation in expression of "Detection of phase variation" of phase variation in expression of "Detection of phase variation" of "Detection of phase variation" of phase variation in expression of "Detection of phase variation" of phase variation in expression of "Detection of phase variation" of phase variation in expression of "Detection of phase variation" of phase variation in expression of "Detection of phase variation" of phase variation in expression of "Detection of phase variation" of "Detection of phase variation" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Detection" of "Det
                                  InterPro; IPR000531; TonB boxC.
Pfam; PF00593; TonB boxC; 1.
PROSITE; PS00430; TONB DEPENDEN'
PROSITE; PS01156; TONB DEPENDEN'
PROSITE; PS01156; TONB DEPENDEN'
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                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                      EMBL; AF221060; AAF80178.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                          IS REQUIRED FOR HEME UPTAKE.

IS REQUIRED FOR HEME UPTAKE.

SUBCELLULAR LOCATION: OUTET membrane.

MISCELLANEOUS: THIS PROTEIN IS SUBJECT TO PHASE-VARIABLE EXPRESSION ASSOCIATED WITH ALTERATION IN THE LENGTH OF THE CCAA REPEAT REGION. THIS MECHANISM IS CALLED SLIPPED-STRAND MISPAIRING. ADDITION OR LOSS OF CCAA REPEAT UNITS WOULD CHANGE THE READING FRAME AND RESULT IN INTRODUCTION OP STOP CODONS DOWNSTREAM OF THE REPEAT REGION. THIS MAY BE A MECHANISM OF REGULATION AND A WAY TO AVOID THE INMINOLOGICAL RESPONSE OF THE HOST.

SIMILARITY: BELONGS TO THE TONB-DEPENDENT RECEPTOR PROTEIN FAMILY;
                                                                                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                  HEMOGLOBIN/HAPTOGLOBIN BINDING PROTEIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN
                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTPE-----AMAAYRFTPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immun.
PS00430; TONB DEPENDENT REC 1; FALSE NEG.
PS01156; TONB DEPENDENT REC 2; 1.
mbrane; Transport; TonB box; Multigene family; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding
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(Rel. 40, Last seq
(Rel. 40, Last ann
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40, Last annotation update)
g protein C precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                993
                                                                                                                                                                                                                 noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                          rmatics and the EMBL outst
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Best Local
                                            Q9NYQ8; O75091; Q9NSR7;
Q9NYQ8; O75091; Q9NSR7;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protocadherin Fat 2 precursor (hFat2) (Mult
factor-like domains 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor;
SIGNAL
CHAIN
DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
SITE
HPAT2 OR MEGF1 OR CDHF8.
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                        HUMAN
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                                                                                                                              FAT2
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                                                                                                                                                                                         EGNA-TYGYIGKWRESELETEVLNGRKFARIKDRK-----DKNNRDNR
                                                                                                                                                                                                                                          Q--FKEKGTAADGTKTYDFDTFIDTNNQEIVGKLNLGYANDTWYDCSLFDCKDGTKMKVF
                                                                                                                                                                                                                                                                  HKASKTKFTGYAGA-VYDLN-----DNNSLYLSLSQLYTPQTNLDA------DGKLLKPR
                                                                                                                                                                                                                                                                                                                     VR------GYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTL
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                                                                                                                                                                                                                                                                                            TRARTDEYCDAGVTHCQGTEN------PTGLKLTNG-----KITRRNGTDL
                                                                                                                                                                                                                                                                                                                                                                                                                        PAGRPGCNTADDKACAVGLGTEIKOKALAFDASYSRPFRLGNTAN-EFVIGADYNRFRST
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                                                                                                                           STANDARD;
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HEMOGLOBIN BINDING PROTEIN

X 4 AA TANDEM REPEATS OF
 Craniata; Vertebrata; Catarrhini; Hominidae
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NB C-TERMINAL BOX.

A551BF3B2C641612
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                                                                            update)
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 Hominidae;
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MEDLINE=20202599; PubMed=10716726;
WLO., Maniatis T.;
WLASPE exons encoding multiple ectodomains are a characteristic feature of protocadherin genes.";
Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
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TISSUB=Brain;
MEDLINE=98360089; PubMed=9693030;
MRAYAMM M., NakAjima D., Nagase T., Nomura N., Seki N., Ohara O "Identification of high-molecular-weight proteins with multiple EGF-like motifs by motif-trap screening.";
Genomics 51:27-34(1998).
                                                                                                                                                                                                                                                    PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50025; LAM G DOMAIN; 1.
Transmembrane; GlycopTotein; Repeat; EGF-like domain; Signal.
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HSSP; P00740, 1EDM.
HSSP; P00740, 1EDM.
InterPro; IPR00126, Cadherin.
InterPro; IPR00126, EGF-like.
InterPro; IPR001791; Laminin.G.
Ffam; PP00008; EGF, 2.
PRINTS; PR00208; CADHERIN.
SWART; SW00112; CA, 32.
SWART; SW00112; CA, 32.
SWART; SW00112; CA, 32.
SWART; SW001212; CA, 32.
SWART; SW00122; LamG; 1.
PROSITE; PS00232; CADHERIN_1; 14.
PROSITE; PS00232; CADHERIN_1; 14.
PROSITE; PS00232; CADHERIN_1; 14.
PROSITE; PS00232; CADHERIN_1; 13.
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EMBL; AB011535; BAA32463.1; -.
EMBL; AL157443; CAB75663.1; -.
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the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
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Uchida M., Tanaka H.,
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             noved. Usage by and for commercial (See http://www.isb-sib.ch/announce)
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DOMAIN
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SMART; SM00060; FN3; 2.
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PRODOM; PD000471; Glyco_hydro_18;
SMART: SM00495; ChtBD3; 1.
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PIR; A38368; A38368.
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TGTTATISGLAADTSYTFTVKAK--DAAGNVSAASNAVSVKTAAETTNPGVS-AWQVNTA
                    AGGYATFDAMAA---YRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLR
                                                               TASNSRDDGIFLLMPKHSANLWTTYQVTPELTIG------
                                                                                     NASTDNVGVTGYNVYNGANLATSVTGTTATISGLTAGTSYTFTIKAKDAAGNLSAASNAV
                                                                                                           ----RYAALGKRVMEG--VETEISGAVTPKWQIHAGYSYLH-----
                                                                                                                                 GLGGAMFWELSGDRNKTLQNKLKADLPTGGTVPPVDTTAPSVPGNARSTGVTANSVTLAW
                                                                                                                                                       LNARVSFYRMK-DKN-------AAAPLNPNNKKT------
                                                                                                                                                                              RYWNDTAKVPYLYNASNKRFISYD-----DAE---
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                                          TVSTTAQPGGDTQAPTAPTNLASTAQTTSSITLSWTASTDNVGVTGYDVYNG
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y; IPR001579; ChiTinase 18/2.
y; IPR003961; FN III. -
y; IPR003962; FnTII_repeat.
y; IPR001223; Glyco_hydro_18.
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2004
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2004
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Pred. No. 0.26
47; Mismatches
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CATALYTIC.
FIBRONECTIN TYPE-III (R-
FIBRONECTIN TYPE-III (R-
PROTON DONOR (PROBABLE).
D->N: DECREASE IN ACTIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D->E: NO CHANGE IN ACTIVITY
E->D,Q: LOSS OF ACTIVITY:
; AC7C9B22E2987643 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -: SUBCELLULAR LOCATION: Outer membrane.
-: SUBCELLULAR LOCATION: Outer membrane.
-: MISCELLANBOUS: THIS PROTEIN IS SUBJECT TO PHASE-VARIABLE
EXPRESSION ASSOCIATED WITH ALTERATION IN THE LENGTH OF THE CCAA
REPEAT REGION. THIS MECHANISM IS CALLED SILPPED-STRAND MISPAIRING.
ADDITION OR LOSS OF CCAA REPEAT UNITS WOULD CHANGE THE READING
FRAME AND RESULT IN INTRODUCTION OF STOP CODOUS DOWNSTREAM OF THE
REPEAT REGION. THIS MAY BE A MECHANISM OF TREGULATION AND A
MAY TO AVOID THE IMMUNOLOGICAL RESPONSE OF THE HOST.
-: SIMILARITY: BELONGS TO THE TONB-DEPENDENT RECEPTOR PROTEIN FAMILY;
HENGGLOBIN/MARTOGLOBIN BINDING PROTEIN SUBFAMILY.
-: CAUTION: THIS IS A CONCEPTUAL TRANSLATION, A FRAMESHIFT WAS
INTRODUCED IN THE REPEATS REGION TO MAXIMIZE THE SIMILARITY
WITH OTHER ORTHOLOGS.
                                                                                                                                                                                                                                                                                                                                                       "Identification of an outer membrane protein involved in utilization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: ACTS AS A RECEPTOR FOR THE HEMOGLOBIN/HAPTOGLOBIN COMPLEX OF THE HUMAN HOST AND IS REQUIRED FOR HEME UPTAKE. DOES NOT BIND HEMOGLOBIN ALONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEMOGLOBIN-HAPTOGLOBIN BINDING PROTEIN
                                                                                                                                                                                                                                                                                               STRAIN=NTHI TN106;
MEDLINE=96355882; PubMed=8751920;
Maciver I., Latimer J.L., Liem H.H., Muller-Eberhard U., Hrkal Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X 4 AA TANDEM REPEATS OF Q-P-T-N.
                                                                                                                         i6-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemoglobin-haptoglobin binding protein A precursor (Hemoglobin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, U43198; AAB36696.1; ALT SEQ.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Transport; TonB_box; Multigene family; Signal;
Receptor; Repeat.
                                                                                                                                                                                                                                                                                                                                                                      hemoglobin-haptoglobin complexes by nontypeable Haemophilus
                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
NCBI_TaxID=727;
                                                                                                1046 AA
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                                                                                                PRT;
                                                                                                                                                                                 haptoglobin utilization protein A)
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                                                                                                STANDARD;
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                                                                                                                                                                                                             Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 IGADYNRFRSTNEQGRITLLYARGGLAL--NEFRSIPQVDLIANARKGVRGYSH----TV 439
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P49331; 069383; 069386; 069389; 069398;
01-PEB-1996 (Rel. 33, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Glucosyltransferase-S precursor (EC 2.4.1.5) (GTF-S) (Dextransucrase)
                                                                                                                                                                                      Gарв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GASPRPAEKN--NRHETFYAAADWDINPDTVLGAG-YLYQQRHLAPYNGLPADANNKLPS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 LPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 TPAGRPGCNTADDKACAVGL-GTE-----IKQKALAFDASYSRPFRLGNTANEFV 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440 ATENL----DEFGIYGKSTFHPADGL-----SLIG-GGRLGHYKIESGEGKTLHK---- 484
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                                                                                                                                                                                                                                                                                    5 MSVFRINMTAATVLAALSSSV-FAAQ------TADLETVHIKGQRS 43
                                                                                                                                                                                                                                                                                                                                                                                                                              61 HNDNTPPK-----IAETIKT---AKKPEKEQA------QDVKD------LVRYETGI 97
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                                                                                                                                                                                      Indels 290;
                                                                                                                             3.4%; Score 129; DB 1; Length 1046;
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51 58 TONB BOX.
1029 1046 TONB C-TERMINAL BOX.
1046 AA; 119295 MW; A5D208A68D27A84E CRC64;
                                                                                                                                                      21.1%; Pred. No. 0.46;
tive 97; Mismatches 271;
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REMBL; M2926; AAA26895.1; -.

REMBL; D88653; BAA26107.1; -.

REMBL; D88659; BAA26111.1; -.

REMBL; D88659; BAA26111.1; -.

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REMBL; D89799; BAA2612.1; -.

REMBL; D89799; BAA2612.1; -.

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REMBL; D89790; BAA2612.1; -.

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STRAIN=MT4239,
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NCBI_TaxID=1309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Nucleotide sequence of the Streptococcus the glucosyltransferase-S enzyme."; J. Gen. Microbiol. 136:2099-2105(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in the by single by and for contined and this statement is not removed. Usage by and for contined and this statement is not removed.
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68 A -> S (IN STRAIN.
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113 T -> I (IN STRAINS MT42.
122 MT8148).
132 S -> A (IN STRAINS MT4239, MT-
AND MT8148).
A -> V (IN STRAIN MT4239).
V -> L (IN STRAIN MT4245).
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| 93 RFRSTNEGGRTTLYARGGLALNEFRSI<br> | FRSIPQVDLI             | Db. 332GKKRYFDDGSGNMAVNRFANDKNGDWYYLNSDGIALVGVQTIN 1274 | GGRLGHYKIESGE                    |                          | 479GKTLHKASKTKFTGYAGAVYDLNDNNSLYL-SLSQL 513 |                          | 514 YTPQTNLDAPGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNK 571 | 1395 LTGSQRIN-DQRVFFTREGKQVKGDVAYDERRLLRYYDKNSGNMVYN 1440 | ISGAVTPKWOIHAGY 604                       | : |
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|                                    | 93 RFRSTNEQGRITLYARGGL | 32GKKRYFDDGSGNM                                         | 451 GKSTFHPADGLSLIGGGRLGHYKIESGE | 75 GKTYYFGQDGKQIKGKIITDN | 79KTKPS                                     | 35 QTIAGKKLYFASDGKQVKGSF | 14 YTPQTNLDADGKLLKPRQGNQI                                          | 95 LTGSQRIN-DQRVFFTREGKQY                                 | 572 KTRYAALGKRVMEGVETEISGAVTPKWQIHAGY 604 | 1 |

Search completed: December 18, 2002, 06:42:58 Job time : 29.3071 secs